

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 00:33:43 : Search time 2007.77 Seconds
(without alignments)
10130.938 Million cell updates/sec

Title: US-09-763-329-1
Perfect score: 972
Sequence: 1 tagaataattgtgtgtat.....gcataaagctgcaaaagcct 972

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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10: gb_ro:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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1	972	100.0	2562	8	MZEZEIN10K	M23537 Zea mays 10
2	93.4	9.6	570	8	ZMZEIN10K	X07535 Maize mRNA
3	89.4	9.2	13868	6	AX027357	AX027357 Sequence
4	87.4	9.0	3695	8	ZM27KZNB	X55118 Z. mays 27KD
5	87	9.0	17380	8	AF215823	AF215823 Zea mays
6	80.4	8.3	147198	8	AF466203	AF466203 Zea mays
7	70.4	7.2	1857	8	MZEGLT2E	M10666 Maize endos
8	70.4	7.2	2975	8	ZMGC22EI	X53514 Maize Zc2 g
9	70	7.2	346296	8	AF090447	AF090447 Zea mays
10	69.8	7.2	141939	8	AF466546	AF466546 Zea mays
11	69.6	7.2	140465	2	AF004668	AF004668 Oryza sat
12	69.6	7.2	148138	2	AP004395	AP004395 Oryza sat
13	69.6	7.2	160480	8	AF123535	AF123535 Zea mays
14	68.8	7.1	879	6	AX096997	AX096997 Sequence
15	68.8	7.1	879	6	AX096998	AX096998 Sequence
16	68.8	7.1	147198	8	AF466203	AF466203 Zea mays
17	68.8	7.1	226001	8	AF391808	AF391808 Zea mays
18	68.6	7.1	620	8	AF371266	AF371266 Zea mays
19	67.8	7.0	1644	8	ZM068404	U68404 Zea mays re
20	67.8	7.0	1698	8	AF050440	AF050440 Zea mays
21	67.8	7.0	2661	6	AR007511	AR007511 Sequence
22	67.8	7.0	2661	6	AR084077	AR084077 Sequence
23	66.4	6.8	3735	8	ZMA131535	AJ131535 Zea mays
24	66.2	6.8	3704	8	ZM27KZNA	X56117 Z. mays 27KD
25	66.2	6.8	130843	8	AF464738	AF464738 Zea mays
26	65.8	6.8	5995	8	ZM032636	U32636 Zea mays ph
27	65.6	6.7	143654	2	AP004574	AP004574 Oryza sat
28	65.4	6.7	3196	8	AF465642	AF465642 Zea mays
29	65.2	6.7	10420	8	AF223412	AF223412 Zea mays
30	65	6.7	157920	2	AP003564	AP003564 Oryza sat
31	64.4	6.6	157601	2	AP004662	AP004662 Oryza sat
32	64.2	6.6	4929	8	ZMCAPC4	X73152 Z. mays GAPC
33	63.8	6.6	253305	3	PFMA13P7	AL034559 Plasmodu
34	63.4	6.5	7343	8	ZMA222KD	X61085 Z. mays 22KD
35	63.4	6.5	346296	8	AF090447	AF090447 Zea mays
36	63	6.5	100820	2	AL591365	AL591365 Danio rer
37	63	6.3	168258	8	AP003021	AP003021 Oryza sat
38	60.8	6.3	199551	2	AC006281	AC006281 Plasmodu
39	59.6	6.1	1453	8	AF050439	AF050439 Zea mays
40	59.6	6.1	60605	25	AF320086	AF320086 Zea mays
41	59.6	6.1	115787	8	AF466202	AF466202 Zea mays
42	59.6	6.1	155150	2	OSJN01006	AL607097 Oryza sat
43	59.6	6.1	226001	8	AF391808	AF391808 Zea mays
44	59.2	6.1	157601	2	AP004662	AP004662 Oryza sat
45	59.2	6.1	181581	2	AC026621	AC026621 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS MZEZEIN10K 2562 bp DNA linear PLN 19-JUL-1994
DEFINITION Zea mays 10-kDa zein gene, complete cds.
ACCESSION M23537
VERSION M23537.1 GI:340933
KEYWORDS methionine-rich protein; seed storage protein; zein protein.
SOURCE Zea mays 3-week old seedling leaf DNA.
ORGANISM Zea mays

REFERENCE
AUTHORS Kirihaara,J.A., Petri,J.B. and Messing,J.
TITLE Isolation and sequence of a gene encoding a methionine-rich 10-kDa zein protein from maize
JOURNAL Gene 71, 359-370 (1988)
MEDLINE 89138012

FEATURES
source

1.2562
/organism="Zea mays"
/db_xref="taxon:4577"
/cell_line="inbred BSSS-53"

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/dev_stage="3-week old seedling"
TATA_signal
1044..1050
1082..1085
1137..11589
/note="10 kDa"
/codon_start=1
/product="zein protein"
/protein_id="AAA3541.1"
/db_xref="GI:511870"
/translation="MAAKMLALFALLALCASATSAHPIGHLPVMPDGMNPKOYC
MNOGLASIMACPSIMLOQLALPIQTPVPMPOMTNPMSPMLMPSMSPVLPSPM
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sig_peptide
1137..1199
1200..1586
/note="10 kDa"
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polyA_signal
1653..1660
BASE COUNT 782 a 506 c 471 g 803 t
ORIGIN

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Query Match          100.0%  Score 972; DB 8; Length 2562;
Best Local Similarity 100.0%  Pred. No. 1.5e-165;
Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tagaataattgtgtgtatcgaataatgattgacatgcagctggtgactcatat 60
DB 1591 TAGAATATTGTGTGTTGTTATCGATATATGATTGACATGCCATGGGTGACTCATAT 1650

OY 61 taacaaataaacagcttccctctatctatcttcttcttcttcttcttcttctt 120
DB 1651 TAACATAAAGCAAGTTCTCTTATATCTTTTATATCTCTCCCTATCCATTTTGA 1710

OY 121 aagccatatactccttaccctcctaagtcaccaatatacttgaaccttaattgtat 180
DB 1711 AAGCCATTATCTTACCTTACCTCCCTAAGTCCCAATATATTTTAACTTAAATGTATG 1770

OY 181 atattcaaaagatgcaataaactcagacatatataaaacacataactaaagtatg 240
DB 1771 ATATTCAAAAGATGACATTAATCTAGCATATATATATAACACATTAATTAAGTATG 1830

OY 241 tatgaattctataaaatgctaaacgaactaatatataaggaaggaaggaacttata 300
DB 1831 TATGAATCTATTAATAATGCTAAACGACTAATATATATGAGGAGGAGTACTTTATTA 1890

OY 301 gtagaatatactgtctatcttctctatctccaataataagtcgtcttcttcaatcaat 360
DB 1891 GTAGATTAATCTGTAATTTTCTATCTATCCCAATATAAGTCTGTTTCAATCAATCAAT 1950

OY 361 atatactacatgctccaaacacttgaattatatactcagtgacgacatcgttcagat 420
DB 1951 ATATATTACATGCTCCAAACATTTTGAATATATCTAGTGACGATCCGTCCACGAT 2010

OY 421 gctaaabaagaagcagtcaggtgtctggtcccaaaactaaatcgctcgttgcgtcaacta 480
DB 2011 GCTAAABAAGAGCAGTCACGCTGTGTCCTCCAAACTAATCGCTGTCGTCACCTA 2070

OY 481 taagaattcagaagaacacaaataaaggacataataatataatgataatactcctct 540
DB 2071 TAAAGATTGATGAGAGCAAAATTAAGCAATTAATTAATTAATTAATGATGACTCTCTCT 2130

OY 541 ttctgaattcacttaggaatatacaaaagcaacaaacaaagaaagaaagatcaagtaataaa 600
DB 2131 TTTGAATTACTTAGGAATATACATAGCAAAACAAACAAAGCAAGATCAAGTAAATTA 2190

OY 601 ggcatcttctgagaacaaatggaagacataaagaatgataagtaattgtgtctctt 660
DB 2191 GGCAATTTTGTGAGAAACATGGAACATTAAGATGCAATTAAGATTTGTGCTCTTT 2250

OY 661 atatttttttttcaagtgaaattcaatagataccatcgtggtgtcgtgtaatacaaa 720
DB 2251 ATATTTTATTTTATTCACGTGAATTTACATAGATACCATCGATGTTGATGGTAAATACA 2310

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OY 721 tgatgccttagctccgaagacttcgaatgatgagcatttaaaatactctatcaattg 780
DB 2311 TGATGCTTAGCTCCGAGAGCTTCGAATGATGAGCGATTTAAAAATCTCTATCAATTTG 2370

OY 781 ttctgaagttcttctgtctcatgcatgagcaatglaaccctatttaagaagcgttcgac 840
DB 2371 TTGCAAAAGTTCTTGTCTCATGATGAGCAATGTACGCTATTTATAGGAGCGTCCGAC 2430

OY 841 gtacaaattgtataaataattatatttcaatcccaatccatgataatgtcgtggagac 900
DB 2431 GTACAAATTGTATAAATATATATTTATTCCTCAAAATCCATGATATGTCTCGGAGC 2490

OY 901 ctaattaggggtaccctcaagctcctaattcctaagcttggttaaccataagaataag 960
DB 2491 CTAATTAGGGGTACCCTCAAGCTCCTAATTTCTCAGCTGATACCCATCAGCATTAAG 2550

OY 961 ctgcaaaagcct 972
DB 2551 CTGCAAAAGCCT 2562

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RESULT 2

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ZMZE110K      ZMZE110K      570 bp      mRNA      Linear      PLN 12-SEP-1993
LOCUS         Zea mays
DEFINITION   Maize mRNA for 10kDa zein.
ACCESSION    X07535
VERSION      X07535.1 GI:22540
KEYWORDS     storage protein; zein protein.
SOURCE       Zea mays.
ORGANISM     Zea mays.

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
clade; Panicoideae; Andropogoneae; Zea.

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REFERENCE 1 (bases 1 to 570)
AUTHORS   Kirihara,J.A., Hunsperger,J.P., Mahoney,W.C. and Messing,J.W.
TITLE     Differential expression of a gene for a methionine-rich storage
protein in maize
MOL. GEN. GENET. 211 (3), 477-484 (1988)
MEDLINE    88216260
COMMENT    Data kindly reviewed (20 June 1988) by MESSING J.W.
FEATURES   Location/Qualifiers
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            1..570
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            /strain="W23"
            /db_xref="taxon:4577"
            /clone="10K2-1"
            /tissue_type="endosperm"
            /clone_1fb="pUC119"
            22..474
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570
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BASE COUNT 140 a 151 c 127 g 152 t
ORIGIN

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Query Match          9.6%  Score 93.4; DB 8; Length 570;
Best Local Similarity 98.9%  Pred. No. 1.7e-07;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tagaataattgtgtgtatcgaataatgattgacatgcagctggtgactcatat 60
DB 1591 TAGAATATTGTGTGTTGTTATCGATATATGATTGACATGCCATGGGTGACTCATAT 1650

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Db 476 TAGAATATTTGTGTGTACCGAATATGATGACATGCCATCGCGTGTACTCATTTAT 535
Qy 61 taacaataaacaagttctctcttattatctttt 95
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Db 536 TAACAAATAAACAAGTTTCTCTTATATATCTTTT 570

RESULT 3
AX027357/c 13868 bp DNA linear PAT 16-SEP-2000
LOCUS Sequence 5 from Patent W0037488.
DEFINITION AX027357
ACCESSION AX027357 GI:10188332
VERSION AX027357.1
KEYWORDS
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
AUTHORS Theissen-G., Deley-W., Saedler H. and Cacharron, J.
TITLE Novel mads-box genes and uses thereof
JOURNAL Patent: WO 0037488-A 5 29-JUN-2000;
MAX PLANCK GESELLSCHAFT (DE)
FEATURES
source 1. 13868
/organism="Zea mays"
/db_xref="taxon:4577"
BASE COUNT 4120 a 2725 c 2718 g 4305 t
ORIGIN

Query Match 9.2%; Score 89.4; DB 6; Length 13868;
Best Local Similarity 67.4%; Pred. No. 4.8e-07;
Matches 126; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 128 ttatccttactccctgaagcccaataatatttagaccttaattgtatgtctatattca 187
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Db 12732 TAATACTCCCCATCTTAATAATAGTATTCGCTTAGCTCTCAATTTTATGCTATATCA 12673
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Qy 188 aaagaagacaataatcttgcacataataaaccacataacattgaattgtatgaat 247
|||||
Db 12672 AATAGATGATGATTAATCAACATATTAATAACATTAATCAAGTATGATGATCAAT 12613
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Qy 248 ctattaaatgcctaaagcactaatattatagggagcggtactttagtattgaattc 307
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Db 12612 CTATTTATTTTAAACCAATTTTATTTGGCAAGAGATATATGAGAAATTACAG 12553
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Qy 308 acattgt 314
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Db 12552 AACATGT 12546

RESULT 4
ZM27K2NB/c 3695 bp DNA linear PLN 10-FEB-1992
LOCUS Z.mays 27kda zein locus DNA.
DEFINITION X56118
ACCESSION X56118
VERSION X56118.1 GI:22100
KEYWORDS zein protein.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
AUTHORS Das, O.P., Ward, K., Ray, S. and Messing, J.
TITLE Sequence variation between alleles reveals two types of copy
JOURNAL Genomics 11 (4), 849-856 (1991)
MEDLINE 92147128
REFERENCE 2 (bases 1 to 3695)
AUTHORS Messing, J.

TITLE Direct Submission
JOURNAL Submitted (24-SEP-1990) J. Messing, Rutgers State University,
WAKSMAN INSTITUTE, HOES LANE, PISCATAWAY NEW JERSEY 08855, USA
FEATURES
source Location/Qualifiers
1. 3695
/organism="Zea mays"
/strain="A18"
/db_xref="taxon:4577"
/tissue_type="leaf"
misc_signal 2195..2205
TATA_signal 2448..2451
misc_feature 2482..2484
BASE COUNT 1115 a 877 c 734 g 969 t
ORIGIN

Query Match 9.0%; Score 87.4; DB 8; Length 3695;
Best Local Similarity 79.8%; Pred. No. 1.4e-06;
Matches 103; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 171 ttgtatgtctatattcaaaagatgacaataatcttagacatatataaacaacataca 230
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Db 3501 TTTTGTCTATTAATCAAAATGATGATTAACAAATCTAGATATATAGAAAAACACATATA 3442
|||||
Qy 231 ttaagatgttatgaatcattataaagcttaaaacgacactaatatagggagcgagga 290
|||||
Db 3441 TAAATTTGTTAATTAACCTTAATAAGGTTTAATAAGATTTTAATTTGGACAGATGCGAG 3382
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Qy 291 tacttatt 299
|||||
Db 3381 TATTTTATT 3373

RESULT 5
AF215823 17380 bp DNA linear PLN 02-JAN-2001
LOCUS Zea mays T cytoplasm male sterility restorer factor 2 (rf2) gene,
DEFINITION rf2-873 allele, complete cds.
ACCESSION AF215823
VERSION AF215823.1 GI:12004293
KEYWORDS
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
AUTHORS Cui, X., Hsia, A.P., Wise, R.P. and Schnable, P.S.
TITLE Alternative transcription start sites and polyadenylation sites are
JOURNAL Recruited during Mu Suppression at the rf2 locus of Maize
Unpublished
REFERENCE 2 (bases 1 to 17380)
AUTHORS Hsia, A.P., Chen, W. and Schnable, P.S.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-1999) Agronomy, Iowa State University, G405
Agronomy Hall, Ames, IA 50011, USA
FEATURES
source Location/Qualifiers
1. 17380
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/chromosome="9"
/map="between umc153 and su1"
10..465
/note="similar to 3' LTR of Zea mays retrospoon Mlt"
2065..3096
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and sequence 5' to GmPC4 coding region"
join(3120..3472,5369..5515,6042..6184,6272..6425,
6533..6762,13928..14017,14115..14288,14381..14518,
14863..15000,15119..15180,15304..15869)

[illegible]

REFERENCE AUTHORS JOURNAL TITLE	FEATURES
<p>AUTHORS Ramakrishna,W., Sammiquel,P., Emberton,J. and Bennetzen,J.</p> <p>TITLE Direct Submission</p> <p>JOURNAL Submitted (07-Jan-2002) Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA</p> <p>AUTHORS 2 (bases 1 to 147198)</p> <p>TITLE Llaça,V., Linton,E.W., Young,S., Kovchok,S. and Messing,J.</p> <p>JOURNAL Direct Submission</p> <p>TITLE Submitted (07-Jan-2002) Rutgers, The State University of New Jersey, The Plant Genome Initiative at Rutgers - Waksman Institute, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA</p>	<p>Location/Qualifiers</p> <p>1..147198</p> <p>/organism="Zea mays"</p> <p>/cultivar="B73"</p> <p>/db_xref="taxon:4577"</p> <p>/chromosome="2"</p> <p>/map_pos:"2S: 2.03"</p> <p>/clone="ZMMBBC_0092E12"</p> <p>/join("5148..5420,5843..5923,6003..6658,6741..7344,7419..7764,7846..>8336)</p> <p>/gene="2092E12.1"</p> <p>/product="putative RIRE2 orf3"</p> <p><5148..>8336</p> <p>/gene="2092E12.1"</p> <p>/note="Similar to Zea mays RIRE2 orf3 GB:AF391808.2 GI:17082476"</p> <p>/evidence="not_experimental</p> <p>/join(5148..5420,5843..5923,6003..6658,6741..7344,7419..7764,7846..8336)</p> <p>/gene="2092E12.1"</p> <p>/codon_start=1</p> <p>/evidence="not_experimental</p> <p>/product="putative RIRE2 orf3"</p> <p>/protein_id="AAL75972.1"</p> <p>/db_xref="GI:18568235"</p> <p>/translation="MGGAPSPPPGCVVSVSEHKEGCVTGTRPMRIMHYVELH LTPNLSISQAIFVAVCEGYLGIAPIHMDLWHLPEAFELPTEERKVSAMGKPDISI AFSDLRMRPDGCVTLLEVGWGPSTLPVPEDDAAGAAARVAAKFKKKDKAEKARAR RRKRALDEKCRROOEREGLRPSPSPEDDDDDDDDECDMAARLGLSPGLCGGQ PSSQPSGPPVPVPGVAGSGSPMPARGRPERSPPDSAGVAGVAREGVRASAPGPP VPAHGSDPOVILVPPSPARASAKAVAPRLPKRSSAAVSGAGCTETSQAQRHMA RSCGRSGQTDLPARKKLKTASVCASAPGVVQPTLDSGVSPQGAASVSGEQVPA EAGSSAEAAIYIGCAAGAVVSPLVVPAMIAAPATEVAAVAGVERPVAASGVAAV APASVEEVAGVGRSVQAGDLSIIVARSSEARQDLIRFTRASDPVILDEQEDDS DELERAERATGVSRLSSLEVCGRDVPILDQITRSKASSEFICEVDVMSLSLRK SLDQATRIASQDDAKVADLIQCLADLRBAEAAACAPKOROSSEVQVVEEEDSGRGA VEASRAETLAADIAAQAVASSEGRARAGELESALDSKAKIALAALGAAARQADLA AMSAASDVYRILISGDVPSGSSPQSIQALAGDYARKIRFALHHGVRRAIVLASHV VLDIERVSEGYCLPDEDEDAALAEVQRLDVAAGPSAALATTFEAEILPPAPSLAEADV LITDGDTEGGAAPSGCGA"</p> <p>6215..6254</p> <p>/rpt_unit=cga</p> <p>/evidence="not_experimental</p> <p>/complement("c9301..>12549)</p> <p>/gene="2092E12.2"</p> <p>/product="putative gypsy-type retrotransposon RIRE2"</p> <p>/complement("c9301..>12549)</p> <p>/gene="2092E12.2"</p> <p>/note="similar to gypsy-type retrotransposon RIRE2 GB:AP002881.2 GI:11967907 (Oryza sativa)"</p> <p>/evidence="not_experimental</p> <p>/complement("c9301..12549)</p> <p>/gene="2092E12.2"</p> <p>/codon_start=1</p> <p>/evidence="not_experimental</p> <p>/product="putative gypsy-type retrotransposon RIRE2"</p> <p>/protein_id="AAL75973.1"</p> <p>/db_xref="GI:18568236"</p> <p>/translation="MGSLOQPLDPGTVLRGSLSEFMSLDGSGYGMILPPRDSNGGR RPARRRNRHRLPRMVEQHSSSPLPEPRORRRRGQGGAGGASSAVEETIDIPSA TGGVSGDIALFETKASAVPPRIHAFEMODASALAELOVALVPLKTTTQSVDPYTG LVDOKLITDSHPTSPRLGNPSDEALACALVEASATPLGFRNRSWMDRLIVDTYVG PNSSEEDDDDSICWDFSGFNPSAMPRLACVCLSDCSGSSRSFPDEDCGPERECF</p>

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DEGAGALESIRDVGVWAGQAPARERHLPQGFQHRVANDVVRPPSPSSGOMLA
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WEASVYGTGRNTAPAPAGHLGNHHRDRALDERRGVYPRRGDGEDSDSP
SPSPGQAFSRAIRAPPARPRPTTITKYSGERPELMADYRLACOLGCTDDN
LITRNLPLFSLDTRAMLEHLPPQGISNMDLVQAFAGNFQGYVRPNSWDLRSCRO
QPELSLQYIRRSKQRTLELPTNDSVDVIGALTTCDLVSKLRKPTPTASLMD
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VDMSSVAGADAPFHGILPGKRVQPLGLDPLVCFGPSPNRRRTLTFFEVVFGTHT
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NLCEMDYVQPLEDAIMDGSNFEPSSALPDSASRATSPVAMTMRSSCSG
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RNGCITPLTRFVWT"
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/product="putative gag protein"
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/gene="Z092E12.9"
/note="similar to maize retrotransposon Opie-2 gag gene
GB:U68408.1 GI:1657766"
Query Match 8.3%; Score 80.4; DB 8; Length 147198;
Best Local Similarity 98.8%; Pred. No. 1.3e-05;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 891 tttcggggaccataatgaagggtaccctcaaggtcctaattctcagctggtaccat 950
|||||
Db 14327 tttcggggaccatratatttaggggtaccctcaaggtcctaattctcagctggtaccat 14268
QY 951 cagcataaagctgcaagagcct 972
|||||
Db 14267 cagcatraaacctgcgaagagcct 14246
RESULT 7
MZEGU72E/c 1857 bp DNA linear PLN 27-APR-1993
LOCUS MZEGU72E 1857 bp DNA linear PLN 27-APR-1993
DEFINITION Maize endosperm glutelin-2 gene, complete cds.
ACCESSION M16066
VERSION M16066.1 GI:168484
KEYWORDS glutelin.
SOURCE Maize (Inbred line W64A) DNA and cDNA to mRNA.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1857)
Boronat,A., Martinez,M.C., Reina,M., Puigdomenech,P. and Palau,J.
Isolation and sequencing of a 28 kd glutelin-2 gene from maize:
Common elements in the 5' flanking regions among zein and glutelin
genes
JOURNAL Plant Sci. 47, 95-102 (1986)
COMMENT Draft entry and computer-readable copy of sequence in [1] kindly
provided by A.Boronat, 04-AUG-1987.
There are three potential polyadenylation signals located at
positions 138 to 1343, 1392 to 1397 and 1405 to 1410.

TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2001) Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08854-8020, USA
REMARK	Sequence update by submitter
REFERENCE	5 (bases 1 to 346296)
AUTHORS	Song, R., Llica, V. and Messing, J.
TITLE	Direct Submission
JOURNAL	Submitted (24-APR-2001) Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08854-8020, USA
REMARK	Amino acid sequence updated by submitter
COMMENT	On Apr 12, 2001 this sequence version replaced gi:4416300 gi:4416303.
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RNA	join<11112..11154,11262..11396,12254..12344,14272..14410,14838..14890,18185..18230,18589.>>18657) /product="hypothetical protein" join(11112..11154,11262..11396,12254..12344,14272..14410,14838..14890,18185..18230,18589..18657) /codon_start=1 /evidence=not_experimental /product="hypothetical protein" /protein_id="AAD20311.1" /db_xref="GI:4416306" /translation="MDVGNRPMTATPATRVDERESRAHGDGLTGMSGVAETAETHTGGG
CDS	

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repeat_region	15142..17012 /note="similar to cell division protein FtsZ"
misc_feature	22068..22142 /rpt_type=dispersed
repeat_region	24303..24307 /note="sequence target duplication"
misc_feature	24306..31758 /rpt_family="zeon-1 retroelement"
LTR	/rpt_type=dispersed
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	FLDKSGTQETLKGFLRAQNEFLRKIKIRSDIGTFKNSQIESLEEBGKIKHES				
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	SYELTEGKPNISYFRVFGSKCEFLIKRGRSKPAEAVTGFLAIGDYNRAVFNK				
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	HPHVAIQRDHPVDITLDLHGKVTTRSVARHCENYSVSSIEPRHVAIQRDHP				
	VYVMOEELNFTREYVHILYPRPNQNVYKTRVPRNKNODEGVYTRKRAIKVAGYSQ				
	VEGDGETTAIPVARESLITLAVATYHGRKLYOMVKSAPFNGPILKEEYVBOPG				
	FEESEYPRNHYRLSKALYGLQAFAWAYECLROELINAGRVGADPTLEPKTLENL				
	PCVQIYVDIDIFPGSTNKSCEESFRIMTQGEEMSMQELKYFLFGYKLOEGEFLICQ				
	TKTQDILTKFGMKMDAKPIKTPMCTNHLDLDTGCKVVDQYRSMISGLLYLCASPR				
	DIMLSGCMARQPSQDPESHUTAKRLIYRLATYPRKGLYVPRSGFTLDIGYSDAPMA				
	GCKINRSTSCQCFLOFLRSIYVSNASKNNVATLSTAEVYIAHCOAOILMMQRTLL				
	DYGLTKLVPLLCQDNESAIRKMDNPVZHSRTKHIAIRHFLRDHQKGDIEITINTK				
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Y	884 gcatactgctcgaggaccataattagggtacccctcaagctcctaattctcagctgta	943			
Db	301358 GCAAAATGTCGGGACCATATTAGGGGTACCCCTCAAGAGCCCAATTCCTAGCTGGTA	301417			
Y	944 a-ccccatcagcataaagctcaagaagcct	972			
Db	301418 ACCCCATCAGCATTAAGCTCAAGAAGCCT	301447			
RESULT 10	AF466646	141939 bp	DNA	linear	PLN 07-FEB-2002
AF466646/c	LOCUS	DEFINITION	zea mays clone ZMBB2199D10 putative transposase gene, partial		
			cds; g1yyl-cRNA synthetase, ornithine carboxyltransferase,		
			putative gag protein, putative SET-domain transcriptional		
			regulator, putative oxysterol-binding protein, putative		
			polyprotein, putative oxysterol-binding protein, putative gag-pol		
			polyprotein, putative phosphatidylinositol-4-phosphate-5-kinase,		
			hypothetical protein, putative gag-pol polyprotein, putative		
			polyprotein, putative retrotransposon protein, and pipol genes,		
			complete cds, and putative teosinte branched2; Tst gene, partial		
			cds.		
ACCESSION	AF466646				
VERSION	AF466646.1	GI:18568260			
KEYWORDS					
SOURCE	zea mays.				
ORGANISM	zea mays.				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC				
	clade; Panicoideae; Andropogoneae; Zea.				
REFERENCE	1 (bases 1 to 141939)				
AUTHORS	Ramakrishna, W., Emberton, J., SanMiguel, P. and Bennetzen, J.				
TITLE	Direct Submissions				
JOURNAL	Submitted (07-JUN-2002) Department of Biological Sciences, Purdue				
	University, West Lafayette, IN 47907, USA				
	2 (bases 1 to 141939)				
AUTHORS	Dooley, J.				
TITLE	Direct Submission				
JOURNAL	Submitted (07-JUN-2002) Genetics Department, University of				
	Wisconsin, Madison, WI 53706, USA				
	3 (bases 1 to 141939)				
REFERENCE					

AUTHORS
 Ilaça, V., Linton, E.W., Young, S., Kovchok, S. and Messing, J.
 Direct Submission
 Submitted (08-JAN-2002) Rutgers, The State University of New
 Jersey, The Plant Genome Initiative at Rutgers - Waksman Institute
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 Location/Qualifiers
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 VYTPSPFLMHLFVKAIAHLKRYANDHIRKIVDPMIDRKYKRYRNIPILXSAFILI
 PRKMGESRLVRLRLMNLSTDIAYVOTYTRAKLIDYINIKTEKYGSRVLRNPP
 SCKRSRWAMEIYDDADVGTSGVMSFASLTINARDVSAPALLHAASSASTSELIL
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 /db_xref="GI:18568262"
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 DEIGVEFVAMSTVITIRERDQKQIVNDINEVASVK"
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 10092. .10260,10670. .11003,11514. .11646,11937. .>12056)
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 chloroplast product GB:AF035662.1 GI:6578123"
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Matches 82; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db 8479 TTTGTGGGCGACCAATATTAGGCTACCCTCACAAGCCCTTAATTCACGTGTAACCCC 8420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 948 catgaagcataagctgcacaagcct 972
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8419 CATCAGCACAAAGCTGCAAAAGGCCCT 8395

RESULT 11
AP004668

LOCUS AP004668 140465 bp DNA linear HTG 24-JAN-2002

DEFINITION Oryza sativa chromosome 7 clone P0475E07, *** SEQUENCING IN

ACCESSION AP004668

VERSION PROGRSS ***, in ordered pieces.

KEYWORDS AP004668.1 GI:18307746

SOURCE HTG: HTGS PHASE2.

ORGANISM Oryza sativa (cultivar:Nipponbare) DNA, clone:P0475E07.
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriarthoideae; Oryzaceae; Oryza.
1 (bases 1 to 140465)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (23-JAN-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kannondai
2-1-7, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tssak@nias.affrc.go.jp, URL:http://rpp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

REFERENCE 1
AUTHORS NOTE: It currently consists of 1 contigs. Gaps between the contigs
TITLE are represented as runs of N. The order of the gaps is believed
JOURNAL to be correct as given, however the sizes of the pieces between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
COMMENT * NOTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
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ORIGIN		

Query Match	7.28;	Score 69.6;	DB 2;	Length 140465;
Best Local Similarity	57.38;	Pred. NO. 0.0011;		
Matches 126;	Conservative 0;	Mismatches 94;	Indels 0;	Gaps 0;

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Qy		

Db 80152 CATATCATAGAGCTTCTAGCCCTTCATCCCTCCTCTAGATTACATTAACATCATATTTA 88211

Qy 203 atctgacatctatctaaacacatcatctgaacatgcaagatcgaatccctctaaacacgcga 202

Db 88212 ATTTGACACAAATATATAAGCACATACATAGATCTATGCATGAGTTTATGAAAACCAA 88271

Oy 263 aacgactaataattatgagcagcagaggtacttattagt 302
 |||||
 Db 88272 AACGCTTGGATCTAAACAGACGAACTAATATTAAGT 88311

RESULT 12
AP004395

DEFINITION
Oryza sativa chromosome 7 clone P0030H06, *** SEQUENCING IN
PROGRES *** , in ordered pieces.
ACCESSION
AP004395

KEYWORDS	HTG; HTGS_PHASE2.
SOURCE	Oryza sativa (cultivar:Nipponbare) DNA, clone:FP0030H06.
ORGANISM	Oryza sativa

REFERENCE
1 (bases 1 to 148138)
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

TITLE Direct Submission
JOURNAL Submitted (05-DEC-2001) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kannonda

COMMENT
(E-mail: tsasakigentas.a@irc.go.jp, URL: <http://rpg.dna.irc.go.jp/>)
Tel.: 81-298-38-7441, Fax: 81-298-38-7468
NOTE: It currently consists of 1 contigs. Gaps between the contigs

sequence will be replaced by the finished sequence as soon as it is available. The sequences are based on estimates that have provided the sizes of the gaps between them to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available.

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* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and

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FEATURES
source      Location/Qualifiers
1. 148138   /organism="Oryza sativa"

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/db.xref="taxon:4530"  
/chromosome="7"  
/clone="P0030H06"
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ORIGIN

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Beat LocalSimilarity 57.38; Pred. No. 0.0011;
Matches 126; Conservative 0; Mismatches 94; Indels 0; Gaps 0

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QY	83	cttaacgttttttatatctcccccacatcttttgcgaagccattcccttaaccc	142
Db	15174	TTGGTGATGTTTATTAATTCCTCTCTCTTTTAAATCTGTCTATTAACCTCCGCAATTC	15233
QY	143	taadgcccaatataltttagaccttaaatcgtatgctcatatccaaagaatgcacataa	202
Db	15234	CATATCAATAAGACGCTTCAGCCCTTCATCCCTCCCTCTAGATTTGCTCAATCAATATATTA	15293
QY	203	atctagacatatataaacaactaacctttagctctcttatgaactcttaanaatgctaa	262
Db	15294	ATTTCGAAACCAAAATTAAGACCATACATATAGTCTATGCATGAGATTTTATTGAAACCCAA	15353
QY	263	aacgactaatatlatgagacgagaggaagtaacttlatltagt 302	
Db	15354	AACGCTTGGAATGTAAACAGSAGSAGCACTAATATTAAAGT 15393	

AF123535/C
RESULT 13
160480 bp
149997
DNA
149997
PLN 19-MAR-2000

DEFINITION	Accession
zeamays alcohol dehydrogenase 1 (adult) gene, clone Zm123535	AF123535
complete cds.	AF123535
Accession	AF123535

KEYWORDS .
SOURCE .
ORGANISM .
 Zea mays.
 Zea mays
 wheat (*Triticum aestivum*).
 Charophyta; Embryophyta; Tracheophyta.

REFERENCE

1. (bases 1 to 160480)

TITLE
Bennetzen, J. L. and Avramova, Z.
Collinearity and its exceptions in orthologous adh regions of maize
and sorghum
1993 1: 541-547. P. 541. 05 (13) 7400-7414 (1993)

PUBMED	103//428
REFERENCE	2 (bases 1 to 160480)
AUTHORS	Sanmiquel, P. J., Tikhonov, A. and Bennettzen, J. L.

FEATURES
JOURNAL
Submitted (25-JAN-1995) biological sciences, Purdue University,
Hansen LSRB, Rm. 339, West Lafayette, IN 47907, USA
Location/Qualifiers
100000

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/organism="Zea mays"
/db_xref="taxon:4577"
/clone="VAC 334B"
190707 190713 190640 190746 190702 190208 190

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20552.  .20713,20814.  .>20930)
/genex="adh1"

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	19648	19746	19703 19708

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19620. 19702,19795. .19870,.20216. .20217,.20363. .20460,
20552. .20713,.20814. .20930)
/gene="adh1"

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/codon_start=1
/product="alcohol dehydrogenase 1"
/protein_id="AAF43977.1"
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/translucency - MATAKRVLICNAAVYEAAGNLSLEEVAVAPADLRVAVLE
 SLCHTDVYEMEARKQTPVPFPRIFKCHAGAILIESGEGVWDVAPADHVLVFTGCEKEE
 AHCKSAESNMCDLIRINTDRCGMADGKRSFINSKPRITHEVGSTSEFETVMHGG

ASRIIGVLDNPSRREEARKEPVGEVLAEMINGVUDSVELGON I
AMIOFECVHDGQVAVALGVPHKDAEFPHPMFLNERLKLCTFFGNGYKPRDLPN
VELYMKKELEVEKEFTTHSVFPAELINKAFDLMARKEGIRCLIRMEN"

...

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 00:45:13 ; Search time 201.54 Seconds
(without alignments)
8280.445 Million cell updates/sec

Title: US-09-763-329-1

Perfect score: 972
Sequence: 1 tagaataattgtgtgtat.....gcataaagctgaagagcct 972

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_032802:.*
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	972	100.0	972	21	AAZ93518
2	972	100.0	2562	19	AAV70953
3	89.4	9.2	13868	21	AAA51324
4	82.4	8.5	1203	21	AAC48017
5	69.4	7.1	2710	13	AAQ20749
6	68.8	7.1	879	22	AAF81456
7	68.8	7.1	879	22	AAF81457
8	67.8	7.0	2661	15	AA053873
9	59.2	6.1	4936	24	AA519028

C	10	56	5.8	17594	24	ABL34027	Human immune syste
C	11	54.2	5.6	631	22	AAF81465	Corn promoter clon
C	12	54.2	5.6	2722	21	AAC86507	DNA construct a b
C	13	54.2	5.6	2722	21	AAC86508	DNA construct comp
C	14	54.2	5.6	3991	22	AA016633	Human novel protei
C	15	54.2	5.6	5173	20	AA208721	Chimeric gene cons
C	16	54.2	5.6	5392	20	AA208720	Chimeric gene cons
C	17	54.2	5.6	5622	21	AAC86506	DNA construct comp
C	18	52.8	5.4	8576	24	ABL34228	Human immune syste
C	19	52.6	5.4	5360	20	AA208717	Chimeric gene cons
C	20	51.6	5.3	2418	13	AA027886	P.falciptarum GBP13
C	21	51.2	5.3	8375	24	ABL33079	Human immune syste
C	22	51	5.2	5427	24	ABL32713	Human immune syste
C	23	50.4	5.2	2437	24	ABL34350	Human immune syste
C	24	50.4	5.2	15649	22	AA545396	Chemically pretrea
C	25	50	5.1	6092	24	ABL33271	Human immune syste
C	26	49.8	5.1	5379	24	ABL33677	Human immune syste
C	27	49.8	5.1	5379	24	ABL34577	Human immune syste
C	28	49.8	5.1	18154	24	ABL32254	Human immune syste
C	29	49.2	5.1	1428	21	AAA99466	Sakuranetin syntha
C	30	49.2	5.1	4371	21	AAA99469	Sakuranetin syntha
C	31	49.2	5.1	5241	21	AAA99467	Sakuranetin syntha
C	32	49	5.0	8210	24	AA561283	Human gene regulat
C	33	48.4	5.0	6503	24	ABL32770	Human immune syste
C	34	48.4	5.0	19659	24	ABL32766	Human immune syste
C	35	48.2	5.0	15548	24	ABL34155	Human immune syste
C	36	47.8	4.9	5518	18	AA073870	Cotton fibre promo
C	37	47.8	4.9	5547	18	AA073865	Cotton fibre promo
C	38	47.8	4.9	17869	24	ABL32105	Human immune syste
C	39	47.4	4.9	9483	24	ABL32376	Human immune syste
C	40	47.4	4.9	9483	24	AA561091	Human gene regulat
C	41	47.2	4.9	5945	24	ABL32085	Human immune syste
C	42	47.2	4.9	17280	22	AA546771	Tumour suppressor
C	43	47.2	4.9	17389	24	ABL33414	Human immune syste
C	44	47.2	4.9	61020	22	AA546788	Tumour suppressor
C	45	47	4.8	6065	24	ABL32505	Human immune syste

ALIGNMENTS

RESULT 1	
AAZ93518	standard; DNA; 972 BP.
ID	AAZ93518
XX	AAZ93518;
AC	24-JUL-2000 (first entry)
XX	
DT	24-JUL-2000 (first entry)
XX	
DE	dzrl gene 3' UTR region.
XX	
KW	Maize; corn; methionine; zein storage protein; delta zein; dzrl;
KW	transgenic plants; gene expression; promoter; UTR;
KW	untranslated region; ss.
XX	
OS	Zea mays.
XX	
PN	WO200012681-A1.
XX	
PD	09-MAR-2000.
XX	
PF	25-AUG-1999; 99WO-US20308.
XX	
PR	27-AUG-1998; 98US-0098034.
XX	
PR	07-JUN-1999; 99US-0137836.
XX	
PA	(RUTR) UNIV Rutgers STATE NEW JERSEY.
XX	
PI	Messing J, Lai J;
XX	
DR	WPI; 2000-237865/20.
XX	
PT	DNA construct used for producing transgenic maize plants that express

PT high quantities of 10 kilodalton zein seed storage protein encodes
PT delta-zein operably linked to promoter and to sequence encoding
PT modified 3' untranslated region

Disclosure: Page 48; 54pp; English.

New DNA constructs are described which encode a delta-zeln operably linked to a promoter and to a modified 3' untranslated region (UTR), devoid of binding sites for a drl negative transgenic protein. The DNA construct is useful for producing transgenic maize plants that express high quantities of the 10 kilodalton methionine rich zeln seed storage protein. Overexpression of the zeln storage protein in maize seeds increases the capture of free methionine during plant maturation, which otherwise would be lost. The transgenic plants are superior to prior art natural high-methionine variants because they consistently express the 10 kilodalton transgene regardless of the drl allelic composition of the variety. This sequence is the wild type 3'UTR region of maize prior to modification.

Sequence 972 BP; 329 A; 168 C; 157 G; 318 T; 0 other;

Query Match	100.08;	Score 972;	DB 21;	Length 972;
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Best Local Similarity 100.0%; Pred. No. 3,3e-192;
Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	taaaataatctgtgtgtatcatgaataaaatgaatctgaacatcgatcgcgtgtgactcatat	60
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Db	61	taaaataataaaacaagttccctctctattatctttttataatctccctcatccatttttgc	120
OY	121	aagcccatltaaccttaaccttaaccttaagctcccaataatatttttagacctaaattgatatct	180
Db	121	aagcccatltaaccttaaccttaaccttaagctcccaataatatttttagacctaaattgatatct	180
OY	181	ataatctaaaagaagaataaataaataatctatgaataatataaaacaataatcttaagatttg	240
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OY	241	taataatctataaaatactgaataaaacgaataataataatggagcggaggaagtaattata	300
Db	241	taataatctataaaatactgaataaaacgaataataataatggagcggaggaagtaattata	300
OY	301	gtagatttaactgtgtattttctctatctccaaataataaagttcgttttttcaataatcaat	360
Db	301	gtagatttaactgtgtattttctctatctccaaataataaagttcgttttttcaataatcaat	360
OY	361	ataatctacaatctgcacaaataatcttgaaataataataatgaatctgaatcgcgcgaat	420
Db	361	ataatctacaatctgcacaaataatcttgaaataataataatgaatctgaatcgcgcgaat	420
OY	421	cgtataaaagaagcgcgtccgcggtgtgtgtgtcccaaaaaataatcgtccggtgtgcgtcaacta	480
Db	421	cgtataaaagaagcgcgtccgcggtgtgtgtgtcccaaaaaataatcgtccggtgtgcgtcaacta	480
OY	481	taaaagatctcatgaagaagaacaacaataatgaagcabaataatgaatgaatgaatccctcct	540
Db	481	taaaagatctcatgaagaagaacaacaataatgaagcabaataatgaatgaatgaatccctcct	540
OY	541	cttgaaatctcatgaagaataacataaagaacaacaataaaagaagaagaatcaaggtataataa	600
Db	541	cttgaaatctcatgaagaataacataaagaacaacaataaaagaagaagaatcaaggtataataa	600
OY	601	ggacatcttgagaaagaacaacatgaagaatgcataagtaataatgtgtgtctctt	660
Db	601	ggacatcttgagaaagaacaacatgaagaatgcataagtaataatgtgtgtctctt	660
OY	661	ataatctttttttatctacgcgtgaattatacatagataacatcggatgttcgaatgtaatacaa	720
Db	661	ataatctttttttatctacgcgtgaattatacatagataacatcggatgttcgaatgtaatacaa	720

Accession	Sequence	Position
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Dh	tgatgctcttagctcccgagagacttcgaaatgaatagacgatttaaaatactctataatg	760
Oy	ttcgaaagttctcttgcctcagtcagatcggaagatgtaaccctattataagagacgtcgac	840
Dh	ttcgaaagttctcttgcctcagtcagatcggaagatgtaaccctattataagagacgtcgac	840
Oy	gtacaaatttgtatataaatatatttttatctcccaatccctatgcatagtgtctggagac	900
Dh	gtacaaatttgtatataaatatatttttatctcccaatccctatgcatagtgtctggagac	900
Oy	cataattaggggtaccctcaagagctctcaatctctcagctgtgtaaccctatgataaag	960
Dh	cataattaggggtaccctcaagagctctcaatctctcagctgtgtaaccctatgataaag	960
Oy	ctgcagaagcct 972	
Dh	ctgcagaagcct 972	

RESULT	2
AAV70953	
ID	AAV70953 standard; DNA; 2562 BP.

AAV70953; AC

DT 23-AUG-1999 (first entry)

DE Zea mays 10 kDa zein gene DNA sequence.

Non-glycogen-like polysaccharide production; fermentation; zein gene; starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis; non-starch branching gene; amylopectin; amylose; plant-like starch; ss.

OS Zea mays.

PN WO9844780-A1.

PD 15-OCT-1998.

PF 03-APR-1998; 98WO-US066660.

PR 04-APR-1997; 97US-0042939.

PA (EXSE-) EXSEED GENETICS LLC.

PI Guan H, Keeling PL;

DR WPT; 1998-568285/48.

XX

PT plants - transformed

PT engineered properties

PS Disclosure; Fig 45a;

CC The specification de

CC transforming a host,

CC The specification all

CC involved in product1

CC new starches in plan

CC the course of the in

Sequence 2562 BP; 78

Query Match 100.0%; Score 972; DB 19; Length 2562;
 Best Local Similarity 100.0%; Pred. No. 3,8e-192;
 Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 taacaataaacaagttctccttattatcttttataatctctccatcattttgca 120
 |||||||
 DB 1651 taacaataaacaagttctccttattatcttttataatctctccatcattttgca 1710
 QY 121 aagccattatccttactcccaagtcaccaatatttttagaccttaattatgtct 180
 |||||||
 DB 1711 aagccattatccttactcccaagtcaccaatatttttagaccttaattatgtct 1770
 QY 181 atattcaaaagaaatgacaataatctagacataataaacaacatacattagtattg 240
 |||||||
 DB 1771 atattcaaaagaaatgacaataatctagacataataaacaacatacattagtattg 1830
 QY 241 tatgaatctataaagtctaaacagactaataattatggagcgaggagtactattta 300
 |||||||
 DB 1831 tatgaatctataaagtctaaacagactaataattatggagcgaggagtactattta 1890
 QY 301 gttagattacattgtttttcttattcccaataataagtcgtgtttttcaataccaat 360
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 DB 1891 gttagattacattgtttttcttattcccaataataagtcgtgtttttcaataccaat 1950
 QY 361 atattaccatgtcccaaacatttgattatataatcattagtcagatccgtgcacgat 420
 |||||||
 DB 1951 atattaccatgtcccaaacatttgattatataatcattagtcagatccgtgcacgat 2010
 QY 421 cgttaaaagaagcagtcacggtgtgtgtcccaaaaactaatcgttcgttcgcaccta 480
 |||||||
 DB 2011 cgttaaaagaagcagtcacggtgtgtgtcccaaaaactaatcgttcgttcgcaccta 2070
 QY 481 taagaattcagaaagaaacaaataaaggcaataataatgatatagactccctc 540
 |||||||
 DB 2071 taagaattcagaaagaaacaaataaaggcaataataatgatatagactccctc 2130
 QY 541 ttgtgaattacttagaataacataaagcaaaacaaagaagagaagatcaaggttaataaa 600
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 DB 2131 ttgtgaattacttagaataacataaagcaaaacaaagaagagaagatcaaggttaataaa 2190
 QY 601 ggcattttgtgagaaaacatggaagcatagaaatgcaataatgattgtgtctctt 660
 |||||||
 DB 2191 ggcattttgtgagaaaacatggaagcatagaaatgcaataatgattgtgtctctt 2250
 QY 661 atatttttttattcagatgtaattatcatagatcacatcggttcgattggaataacaa 720
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 DB 2251 atatttttttattcagatgtaattatcatagatcacatcggttcgattggaataacaa 7310
 QY 721 tgaatccttagctcgcagagcttcgaatgataagcgatttaaaaatactcctaactat 780
 |||||||
 DB 2311 tgaatccttagctcgcagagcttcgaatgataagcgatttaaaaatactcctaactat 2370
 QY 781 ttctgaaaagttcttctgtcatatgcatgggcaatgtaacctattataggagcggtcgac 840
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 DB 2371 ttctgaaaagttcttctgtcatatgcatgggcaatgtaacctattataggagcggtcgac 2430
 QY 841 gtacaattttgtataaataattattttatcccaaatcctatgcatatgtgcggggac 900
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 DB 2431 gtacaattttgtataaataattattttatcccaaatcctatgcatatgtgcggggac 2490
 QY 901 cataattagggtgacacctcaaggtccttaattctcagctgtgaaccacatcagcataaag 960
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 DB 2491 cataattagggtgacacctcaaggtccttaattctcagctgtgaaccacatcagcataaag 2550
 QY 961 ctgcaaaagacct 972
 |||||||
 DB 2551 ctgcaaaagacct 2562

RESULT 3
 AA51324/c
 ID AA51324 standard; DNA; 13868 BP.
 XX

AC AA51324;
 XX

DT 26-SEP-2000 (first entry)
 XX

DE 2. mays MADS-box protein ZMM14 gene regulatory sequence.
 XX

KM ZMM14; maize; MIRC-type; MADS-box; DNA-binding; upper floret; spikelet;
 XX

KW inflorescence; grass; chromosome 1; monocotyledon; regulatory region;
 XX

OS disease resistance; flowering; growth regulator; herbicide; OSMADSL; ds.
 XX

PN Zea mays.
 XX

PD WO200037488-A2.
 XX

PF 20-DEC-1999; 99WO-EP10116.
 XX

PR 21-DEC-1998; 98EP-0124335.
 XX

PR 29-OCT-1999; 99EP-0121591.
 XX

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX

PI Cacharron J, Theissen G, Delau W, Saedler H;
 XX

DR WPI: 2000-452177/39.
 XX

PT Novel nucleic acids encoding proteins with the activity of proteins
 expressed in the upper florets of spikelets of grass inflorescences
 useful for producing plants with altered protein levels or
 compositions
 PT

PS Disclosure: Page 88-91; 93pp; English.
 XX

CC This is a regulatory region sequence from the maize (Zea mays) ZMM14
 gene which encodes a MIRC-type MADS-box protein. The protein is involved
 in DNA-binding and is expressed in the upper florets of spikelets of
 CC grass inflorescences. The ZMM8 and ZMM14 genes (see AA51322-23) map to
 CC chromosomes 1 and 9, respectively, and are similar to OSMADSL from rice
 (Oryza sativa). The ZMM8 and ZMM14 genes are useful for study of
 CC MADS-box proteins in monocotyledons. The sequences can be used to
 CC produce transgenic plants having altered level or composition of
 CC protein(s) in the florets of spikelets, for modulating the number of
 CC kernels, for conferring or improving disease resistance, generating late
 CC or early flowering, expressing heterologous proteins in the upper florets
 CC in the spikelets of grass inflorescence, modifying solute partition in
 CC florets, improving kernel derived products or the expression of enzymes
 CC affecting any agronomic aspect of the kernel or the whole inflorescence.
 CC Compounds identified as being activators or inhibitors of genes
 CC specifically expressed in the spikelets of grass inflorescence may be
 CC used as growth regulators and/or herbicides.
 CC

SQ Sequence 13868 BP; 4120 A; 2725 C; 2718 G; 4305 T; 0 other;

Query Match 9.2%; Score 89.4; DB 21; Length 13868;
 Best Local Similarity 67.4%; Pred. No. 2.1e-09;
 Matches 126; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 128 ttatccttaccctcctaagttcccaatataatttaaaccttaattgtatgtctatatca 187
 |||||

DB 12732 TAATACTCCCAATTCGAATAATGATATGCTTACGTCACATTTTATGCTATATCCA 12673
 |||||

QY 188 aaagaatgacaataaactcagacatatataaacaacatataagtaagtatgtatgat 247
 |||||

DB 12672 AATGATGATGATTAATCAACATATATTAATCAACATATTAATCAAGTATGTAAT 12613
 |||||

Oy	248	catcaataatgctaaagacacacatactatgagcagagagagacttattatagatgatt	307
Db	12612	CTATTATTGTTTTTAAAAACGAATTTTAAATTTGGACAAAGAGATATATGAGATTACAAAG	12553
Oy	308	acatctgt	314
Db	12552	AACATCT	12546
RESULT	4		
AAC48017/c			
ID	AAC48017	standard; DNA: 1203 BP.	
XX	AAC48017:		
XX			
XX	18-OCT-2000	(first entry)	
DE	Zee mays DNA fragment SEQ ID NO: 55961.		
XX			
KM	Hybridisation assay; genetic mapping; gene expression control;		
KM	protein identification; signal transduction pathway; metabolic;		
KM	pathway; promoter; termination sequence; corn; ss.		
XX			
OS	Zee mays subsp. mays.		
XX			
PM	EP1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PE	25-FEB-2000; 2000EP-0301439.		
XX			
XX	25-FEB-1999; 9905-0121825.		
PR	05-MAR-1999; 9905-0123180.		
PR	05-MAR-1999; 9905-0123548.		
PR	23-MAR-1999; 9905-0125788.		
PR	25-MAR-1999; 9905-0126264.		
PR	29-MAR-1999; 9905-0126785.		
PR	01-APR-1999; 9905-0127462.		
PR	06-APR-1999; 9905-0128234.		
PR	08-APR-1999; 9905-0128714.		
PR	16-APR-1999; 9905-0129845.		
PR	19-APR-1999; 9905-0130077.		
PR	21-APR-1999; 9905-0130449.		
PR	23-APR-1999; 9905-0130510.		
PR	28-APR-1999; 9905-0130891.		
PR	30-APR-1999; 9905-0131449.		
PR	30-APR-1999; 9905-0132048.		
PR	04-APR-1999; 9905-0132407.		
PR	04-MAY-1999; 9905-0132484.		
PR	05-MAY-1999; 9905-0132485.		
PR	06-MAY-1999; 9905-0132486.		
PR	07-MAY-1999; 9905-0132487.		
PR	11-MAY-1999; 9905-0132863.		
PR	14-MAY-1999; 9905-0134218.		
PR	14-MAY-1999; 9905-0134219.		
PR	14-MAY-1999; 9905-0134221.		
PR	14-MAY-1999; 9905-0134370.		
PR	18-MAY-1999; 9905-0134768.		
PR	19-MAY-1999; 9905-0134941.		
PR	20-MAY-1999; 9905-0135124.		
PR	21-MAY-1999; 9905-0135353.		
PR	24-MAY-1999; 9905-0135359.		
PR	25-MAY-1999; 9905-0136021.		
PR	27-MAY-1999; 9905-0136392.		
PR	28-MAY-1999; 9905-0136782.		
PR	01-JUN-1999; 9905-0137222.		
PR	03-JUN-1999; 9905-0137528.		
PR	04-JUN-1999; 9905-0137724.		
PR	08-JUN-1999; 9905-0138094.		
PR	10-JUN-1999; 9905-0138540.		
PR	10-JUN-1999; 9905-0138847.		
PR	14-JUN-1999; 9905-0139119.		
PR	16-JUN-1999; 9905-0139453.		
PR	16-JUN-1999; 9905-0139453.		
PR	17-JUN-1999; 9905-0139459.		
PR	18-JUN-1999; 9905-0139454.		
PR	18-JUN-1999; 9905-0139455.		
PR	18-JUN-1999; 9905-0139456.		
PR	18-JUN-1999; 9905-0139457.		
PR	18-JUN-1999; 9905-0139458.		
PR	18-JUN-1999; 9905-0139459.		
PR	18-JUN-1999; 9905-0139460.		
PR	18-JUN-1999; 9905-0139461.		
PR	18-JUN-1999; 9905-0139462.		
PR	18-JUN-1999; 9905-0139463.		
PR	18-JUN-1999; 9905-0139750.		
PR	18-JUN-1999; 9905-0139763.		
PR	21-JUN-1999; 9905-0139817.		
PR	22-JUN-1999; 9905-0139899.		
PR	23-JUN-1999; 9905-0140353.		
PR	23-JUN-1999; 9905-0140354.		
PR	24-JUN-1999; 9905-0140695.		
PR	28-JUN-1999; 9905-0140823.		
PR	29-JUN-1999; 9905-0140991.		
PR	30-JUN-1999; 9905-0141287.		
PR	01-JUL-1999; 9905-0141842.		
PR	01-JUL-1999; 9905-0142154.		
PR	02-JUL-1999; 9905-0142055.		
PR	06-JUL-1999; 9905-0142390.		
PR	08-JUL-1999; 9905-0142803.		
PR	09-JUL-1999; 9905-0142920.		
PR	12-JUL-1999; 9905-0142977.		
PR	13-JUL-1999; 9905-014		


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PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148365.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149802.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158222.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 23-OCT-1999; 99US-0160989.
PR 23-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

```

Query Match 8.5%; Score 82.4; DB 21; Length 1203;
Best Local Similarity 70.5%; Pred. No. 4.2e-08;
Matches 110; Conservative 0; Mismatches 46; Indels 0; Caps 0;

```

```

Qy 152 atatatataaacttaagtatctatattcaaaagaatgacataatcttaaga 211
Db 1065 ATTGTGTTAGCTCTTATATATCTATGTCATATTAAATAGATGATGTAATCTAGACA 1006

```

```

Qy 212 tatataaaacacatacattaagtatctatgaatctataaagtctaaacgactaa 271
Db 1005 CATCTATTAAACACATACATCAATATTATATCAATCAACATATCCCAAAAGGAATAG 946
Qy 272 tatatggagcaggaaggatctattatagtagatt 307
Db 945 TAAATCGAGACAGAGGAGTATCTTTGTAATAAAT 910

```

```

RESULT 5
AAO20749
ID AAO20749 standard; cDNA; 2710 BP.
XX
AC AAO20749;
XX
DT 29-OCT-1992 (first entry)
XX
DE Sequence of the promoter region of Zm13, its coding region and 3'
DE flanking region.
XX
RW Pollen-specific promoter; corn; W-22; ss.
XX
OS Zea mays.
XX
FH Key
FT TATA-signal
FT Location/Qualifiers
FT 1282..1287
FT /*tag= a
FT mRNA 1316..1442
FT /*tag= b
FT CDS 1443..2035
FT /*tag= c
FT polyA-signal 2063..2068
FT /*tag= d
FT polyA-site 2325
FT /*tag= e
XX
PN US5086169-A.
XX
PD 04-FEB-1992.
XX
PE 31-OCT-1989; 89US-0429822.
XX
PR 31-OCT-1989; 89US-0429822.
PR 20-APR-1989; 89US-0341151.
XX
PA (UYNV-) UNIV OF NEW YORK.
XX
PI Mascarenhas JP;
XX
DR WPI; 1992-064456/08.
XX
PT Isolated pollen-specific promoter from W-22 corn - used to
PT express genes to inhibit pollen prodn., induce toxicity in pests
PT or enhance nutritional value
XX
PS Claim 8; Fig 2 (a-d); 12pp; English.
XX
XX A cDNA library made to poly(A) RNA isolated from mature pollen of
XX maize was constructed. One of the cDNA clones from the library,
XX Zm13, was selected for detailed characterization. Zm13 represents a
XX gene that is present in a very few copies in the corn genome. It
XX is 929 nucleotides in length and in addition has a 47 nucleotide
XX poly(A) tail. Primer extension analysis indicates that Zm13 is a
XX full length copy of the mRNA, which codes for a predicted
XX polypeptide that is 170 AA residues long and has a mol. wt. of 18.3
XX kD. The hydrophathy profile strongly suggests a signal peptide at
XX the amino terminus. The function of this protein is not yet known.
XX A genomic clone corresp. to Zm13 was isolated by screening a
XX genomic library of the inbred maize line W-22. The cDNA clone is
XX collinear with the genomic clone with no introns being present.
XX
XX Sequence 2710 BP; 720 A; 711 C; 620 G; 659 T; 0 other;

```


OY 332 atataagtcggtttc 347
 11 11 11
Db 410 tattactcgctact 425

RESULT 8

AA053873 standard; DNA; 2661 BP.

AA053873;

27-JUN-1994 (first entry)

Sequence comprising Zm13 promoter of Zea mays.

Maintainer gene; sterile; sterility; homogenous population; hybrid;
seed; fertility restorer gene; pollen lethality gene; Zea mays; ds.

Zea mays.

WO9325695-A.

23-DEC-1993.

11-JUN-1993; 93MO-EP01489.

12-JUN-1992; 92US-0899072.

03-NOV-1992; 92US-0970840.

(PLB2) PLANT GENETIC SYSTEMS NV.

Leemans J, Williams M;

WPI; 1994-007552/01.

Maintainer gene for maintenance of male-sterile plants -
comprises fertility-restorer gene and pollen-lethality gene

Example 1; Page 47-49; 87pp; English.

A maintainer gene of plants, pref. a foreign chimeric gene,
comprises (a) a fertility restorer gene which comprises a fertility
restorer DNA and (ii) a restorer promoter capable of
directing the expression of the fertility restorer DNA and (b) a
pollen lethality gene that is selectively expressed in microspores
and/or pollen of the plant to prevent the production of functional
pollen and which comprises (i) a pollen lethality DNA and (ii) a
pollen specific promoter capable of directing expression of the
pollen lethality DNA. Plants transformed with this DNA (maintainer
plants) can be used to maintain a homogenous population of male
sterile plants for the production of hybrid seed. The Zm13
promoter is a pollen specific promoter and is used in the
construction of a plant transformation vector comprising a
maintainer gene as described.

Sequence 2661 BP; 712 A; 693 C; 603 G; 653 T; 0 other;

Query Match Best Local Similarity 7.0%; Score 67.8; DB 15; Length 2661;
Matches 80; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 891 tgcgggagacataataggggtaccctcaaggctcctaattcagctgtaacc-ca 949
 |||||
Db 2325 tgcgggagacataataggggtaccctcaaggctcctaattcagctgtaacc-ca 949
 |||||
OY 950 tcagcataagctgcgaaggct 972
 |||||
Db 2385 tcagcgtaagctgcgaaggct 2407
 |||||

RESULT 9
AA053873

ID AAS19028 standard; DNA; 4936 BP.
XX
AC AAS19028;

15-MAR-2002 (first entry)

Maize Ramosa 1 coding sequence with insertion mutations.

Maize; Ral; Ramosa 1; meristem identity; branch number; fruit yield;
pollen; zinc finger transcription factor; transgenic plant; mutant; ds.

Zea mays.

Synthetic.

Key Location/Qualifiers
FT misc_signal 2306
 /*tag- a
 /standard_name= "transcriptional start site"

WO200190343-A2.

29-NOV-2001.

22-MAY-2001; 2001WO-US16659.

22-MAY-2000; 2000US-206136P.

(COLD-) COLD SPRING HARBOR LAB.

Marlenssen RA, Vollbrecht E;

WPI; 2002-097651/13.

P-PSDB; AA011823.

New maize Ramosa 1 protein which exhibits zinc finger protein
transcription factor capable of influencing meristem identity and
branch development in plants, useful for improving yield and health of
plants

Claim 16; Fig 11; 90pp; English.

The present invention provides the protein and coding sequences of maize
zinc finger transcription factor Ramosa 1 (Ral). The protein is involved
in the regulation of the plant meristem identity and architecture. The
sequences can be used to produce transgenic plants with a reduced number
of branches which would produce higher yielding primitive plants, and
allow them to be planted at high density, and to produce other plants
with an increased number of branches which would give greater fruit, seed
and pollen yields per plant. The present sequence is a mutated version of
the coding sequence of the invention.

Sequence 4936 BP; 1304 A; 1176 C; 1051 G; 1405 T; 0 other;

Query Match Best Local Similarity 6.1%; Score 59.2; DB 24; Length 4936;
Matches 110; Conservative 0; Mismatches 58; Indels 6; Gaps 1;

OY 129 tctccttaaccctcccaagcccaataatattagaccttaaatgtatgctatataca 188
 |||||
Db 2375 TACTCGCTCCGCTCTTAATAATATTCGTTATGTTTATCTATATTCACA 2316
 |||||
OY 189 aagatgacataaataatcagacataataaacaacataacattatgaatgtatgaac 248
 |||||
Db 2315 ATTAATGATGATTAATCTAGACATATTAACAAT-ATCAAGAAATGTTGAATC 2262
 |||||
OY 249 tattaaatgctaaacagcataatactgagagagagagagacttattagt 302
 |||||
Db 2261 CAATATTCACATAAACAATTTTATTTGGAAACAGAGATATATATAGT 2208
 |||||

RESULT 10
ABL34027/c

```

ID  ABLJ4027 standard; DNA: 17594 BP.
XX
XX  ABLJ4027:
AC
XX  26-MAR-2002 (first entry)
DT
XX
DE  Human immune system associated gene SEQ ID NO: 2000.
XX
XX  Human; immune system disease: cytosine methylation; antiaesthetic;
KW  antiarteriosclerotic; antianaemic; cytosolic; noctropic;
KW  neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW  antipneumatic; antiarthritic; antidiabetic; antipsoriatic;
KW  antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW  acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW  neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW  gene; ds.
XX
XX  Homo sapiens.
OS
XX  WO200200928-A2.
XX
XX  03-JAN-2002.
XX
XX  02-JUL-2001; 2001WO-EP07537.
XX
XX  30-JUN-2000; 2000DE-1032529.
XX  01-SEP-2000; 2000DE-1043826.
XX
XX  (EPIC-) EPICENOMICS AG.
XX
XX  Olek A, Plepenbrock C, Berlin K;
XX
XX  WPI: 2002-130909/17.
DR
XX
XX  Nucleic acid comprising fragment of chemically modified gene, useful
XX  for diagnosis and treatment of diseases associated with abnormal
XX  cytosine methylation.
XX
XX  Claim 1; SEQ ID NO 2000; 32pp + Sequence Listing; German.
XX
XX  The present invention provides a number of human immune system associated
XX  genes which are modified by the methylation of cytosines. The sequences
XX  can be used in the diagnosis and treatment of immune system disorders,
XX  including eye diseases such as retinopathy, neovascular glaucoma and
XX  macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
XX  leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
XX  rheumatoid arthritis, psoriasis and inflammatory/allergative bowel
XX  diseases. The present sequence is a gene of the invention.
XX
XX  Sequence 17594 BP; 5843 A; 96 C; 3426 G; 8229 T; 0 other:
SO

Query Match          5.88; Score 56; DB 24; Length 17594;
Best Local Similarity 46.18; Pred. NO. 0.018;
Matches 261; Conservative 0; Mismatches 300; Indels 5; Gaps 2;

OY  127 attacccttccctcccaagcccaatattcttagacctaaatctgactctatatc 186
DB  14736 ATTATGCCAACCAACATTCTCTTAATCTTTTAAATAATATACATATATATATAC 14677
OY  187 aaaaagatgacataaatactagacataataaacaacatacaatgaagtaactgaa 246
DB  14676 ATATTAATAATCAATTTATATATATATATACCATTAATATATATATATTTCAAT 14617
OY  247 tctattaaaatgcaaacgacatactatgaggaagcgaggaggaacttattagtagat 306
DB  14616 ATTATATTTTATATATATATATATATATATATATATATATATATATATATAT 14557
OY  307 ---taccatgtatatttctctatctatcaataaagtcgtgttttcaatcatcaata 363
DB  14556 ATATATATATTTATATATATATATATATATATATATATATATATATATATAT 14497
OY  364 tatcacatgctcacaacatttgaattatataatactagtgacgaatccgtgcacgaatcgt 423

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DB  14496 AACTTACCTCTAATAAATAAATAATATTATATATATTAACATCTTAATATATAT 14437
OY  424 aaaaagaagcagccagcggtgtgctccaaaactaaatcgctgtcggtcaactataa 483
DB  14436 CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 14377
OY  484 agattcattgagaacccaataaagcgaataataatgaataatgaactcctctt 543
DB  14376 CTCTACTATCTAATAATATCAATAATTAATAACATTAATTAATTAATTAATTA 14317
OY  544 gaattacttgaataaatacaataagcaaaacaaaagagagaatcaaggtaaaataaaggc 603
DB  14316 CAATTAATAATTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 14257
OY  604 attctgtgagaacacatggaagcatalaagaatgcataagtaatgttgcctctata 663
DB  14256 ATACTATATATTAATAA-ATTAATAATAAATAAATAAATAAATAAATAAATAA 14199
OY  664 ttttttattcaagtgaaattacat 689
DB  14198 CATTTTATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 14173

RESULT 11
AAF81465/c
ID  AAF81465 standard; DNA: 631 BP.
XX
XX  AAF81465:
AC
XX  08-JUN-2001 (first entry)
XX
XX  Corn promoter clone #700333814.
XX
XX  Corn; promoter; transgenic plant; herbicide resistance; ds.
XX
XX  Zea mays.
XX
XX  WO200119976-A2.
XX
XX  22-MAR-2001.
XX
XX  13-SEP-2000; 2000WO-US25078.
XX
XX  16-SEP-1999; 99US-0154182.
XX
XX  (MONS ) MONSANTO CO.
XX
XX  Anderson HM, Chay CA, Chen G, Conner TW;
XX
XX  WPI: 2001-244796/25.
XX
XX  Novel promoter nucleic acid sequences useful for regulating
XX  heterologous gene expression in plants, comprising regulatory sequences
XX  located upstream to plant DNA structural coding sequences.
XX
XX  Claim 1; Pages 93-94; 101pp; English.
XX
XX  The present invention relates to novel corn promoter sequences (see
XX  AAF81456-AAF81478). The promoter sequences are useful for conferring
XX  expression of a second polynucleotide molecule in a transgenic plant
XX  tissue. In addition, the promoter sequences are useful for providing
XX  plants with herbicide resistance. The promoter sequences are suitable for
XX  selectively modulating expression of any operatively linked gene and
XX  provide additional regulatory element diversity in a plant expression
XX  vector in gene stacking approaches. The present sequence is one such corn
XX  promoter sequence isolated in the present invention.
XX
XX  Sequence 631 BP; 196 A; 146 C; 120 G; 169 T; 0 other:
SO

Query Match          5.64; Score 54.2; DB 22; Length 631;
Best Local Similarity 78.38; Pred. NO. 0.026;

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Query Match          5.6%: Score 54.2: DB 21: Length 2722:
Best Local Similarity 65.0%: Freq. No. 0.032:
Matches 80: Conservative 0: Mismatches 43: Indels 0: Gaps 0:

Oy 152 atatatcagaacctaaatgtaagtcataatcacaagaatgacaataaactagaca 211
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2561 ATTTGTTTACGATCTTACATTTTTCGTCATATCTAAAGCATGATTAACAATTGCA 2502
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 212 tatatacaaacacacataagtaagtaagtaagtaagtaagtaagtaagtaagtaag 271
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2501 CATATACAGAAACATATTCATATTCATATTCATATTCATATTCATATTCATATTCAT 2442
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 272 tat 274
    |||
Db 2441 TTT 2439

RESULT 14
AADI6633
ID AADI6633 standard: DNA: 3991 BP.
XX
AC AADI6633:
XX
DT 19-NOV-2001 (first entry)
XX
DE Human novel protein-encoding gene 2, SEQ ID NO:60.
XX
XX Human; lipid metabolism protein; neurotropic; neuroprotective; cardiac;
XX cerebroprotective; hepatotropic; antidiabetic; ophthalmic; nephrotropic;
XX immune disorder; autoimmune disease; rheumatoid arthritis; glossitis;
XX systemic lupus erythematosus; conjunctivitis; inflammatory disorder;
XX respiratory disorder; asthma; allergy; CNS disorder; Alzheimer's disease;
XX Parkinson's disease; atherosclerosis; cardiovascular disorder; cancer;
XX coronary disease; familial hypercholesterolemia; hyperlipidaemia;
XX haematopoietic disorder; hypolipidaemia; lipodosis; Gaucher's disease;
XX Tay-sach's disease; mental retardation; gene therapy; antisense therapy;
XX ds.
XX
OS Homo sapiens.
XX
FH key Location/Qualifiers
FT exon 1..101
FT intron /tag= a
FT exon 102..179
FT intron /tag= b
FT exon 180..319
FT intron /tag= c
FT exon 320..2053
FT intron /tag= d
FT exon 2054..2156
FT intron /tag= e
FT exon 2157..3393
FT intron /tag= f
FT exon 3394..3470
FT intron /tag= g
FT exon 3471..3689
FT intron /tag= h
FT exon 3690..3797
FT intron /tag= i
FT exon 3798..3897
FT intron /tag= j
FT exon 3898..3991
FT intron /tag= k
XX
XX WO200155203-A1.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001: 2001WO-US01327.
XX
XX 31-JAN-2000: 2000US-0179065.
XX 04-FEB-2000: 2000US-0180628.
XX 24-FEB-2000: 2000US-0184664.
PR
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PR 02-MAR-2000: 2000US-0186350.
PR 16-MAR-2000: 2000US-0189874.
PR 17-MAR-2000: 2000US-0190076.
PR 18-APR-2000: 2000US-0198123.
PR 19-MAY-2000: 2000US-0205515.
PR 07-JUN-2000: 2000US-0209467.
PR 28-JUN-2000: 2000US-0214886.
PR 30-JUN-2000: 2000US-0215135.
PR 07-JUL-2000: 2000US-0216647.
PR 07-JUL-2000: 2000US-0216880.
PR 11-JUL-2000: 2000US-0217487.
PR 11-JUL-2000: 2000US-0217496.
PR 14-JUL-2000: 2000US-0218290.
PR 26-JUL-2000: 2000US-0220963.
PR 26-JUL-2000: 2000US-0220964.
PR 14-AUG-2000: 2000US-0224518.
PR 14-AUG-2000: 2000US-0224519.
PR 14-AUG-2000: 2000US-0225213.
PR 14-AUG-2000: 2000US-0225214.
PR 14-AUG-2000: 2000US-0225256.
PR 14-AUG-2000: 2000US-0225257.
PR 14-AUG-2000: 2000US-0225258.
PR 14-AUG-2000: 2000US-0225270.
PR 14-AUG-2000: 2000US-0225447.
PR 14-AUG-2000: 2000US-0225757.
PR 14-AUG-2000: 2000US-0225758.
PR 14-AUG-2000: 2000US-0225759.
PR 18-AUG-2000: 2000US-0226279.
PR 22-AUG-2000: 2000US-0226681.
PR 22-AUG-2000: 2000US-0226868.
PR 22-AUG-2000: 2000US-0227182.
PR 23-AUG-2000: 2000US-0227009.
PR 30-AUG-2000: 2000US-0228282.
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PR 01-SEP-2000: 2000US-0229343.
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PR 05-SEP-2000: 2000US-0229509.
PR 05-SEP-2000: 2000US-0229513.
PR 06-SEP-2000: 2000US-0230437.
PR 06-SEP-2000: 2000US-0230438.
PR 08-SEP-2000: 2000US-0231242.
PR 08-SEP-2000: 2000US-0231243.
PR 08-SEP-2000: 2000US-0231244.
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PR 08-SEP-2000: 2000US-0231414.
PR 08-SEP-2000: 2000US-0232080.
PR 08-SEP-2000: 2000US-0232081.
PR 12-SEP-2000: 2000US-0231968.
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PR 14-SEP-2000: 2000US-0232398.
PR 14-SEP-2000: 2000US-0232399.
PR 14-SEP-2000: 2000US-0232400.
PR 14-SEP-2000: 2000US-0232401.
PR 14-SEP-2000: 2000US-0232401.
PR 14-SEP-2000: 2000US-0233063.
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PR 21-SEP-2000: 2000US-0234223.
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PR 25-SEP-2000: 2000US-0234997.
PR 25-SEP-2000: 2000US-0234998.
PR 26-SEP-2000: 2000US-0234984.
PR 27-SEP-2000: 2000US-0235834.
PR 27-SEP-2000: 2000US-0235835.
PR 29-SEP-2000: 2000US-0236327.
PR 29-SEP-2000: 2000US-0236367.
PR 29-SEP-2000: 2000US-0236368.
PR 29-SEP-2000: 2000US-0236369.
PR 29-SEP-2000: 2000US-0236370.
PR 02-OCT-2000: 2000US-0236802.
PR 02-OCT-2000: 2000US-0237037.
PR 02-OCT-2000: 2000US-0237038.
PR 02-OCT-2000: 2000US-0237039.
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DB	3151	ltaataataataataattatttataaatttaataataataataataatttaaat	3210	
QY	117	tgcgaagcccatcactccttactccctgaugcccaattattttgaccttaattgt	176	
DB	3211	ataaaataacatacatcttcaaatctcaataaatalatattcaatttbaaataat	3270	
QY	177	gtcatattccaagaagatgcacataaactgaacacataataaaccacatacattag	236	
DB	3271	atcatatttaatttataataataaatalatatttatatttataaattataattattt	3330	
QY	237	attgtatgaactctatttaaaatgcctaaacgactaatattatggagcggaggaagta	296	
DB	3331	lataaattatataataaatalattatataataatttataaattataattatgtatata	3390	
QY	297	attagatgaattacatgtatattttctctatcccaataataagtcggtttcaatcaat	356	
DB	3391	aataataaataataataattataataaataataataataataataataataataataat	3450	
QY	357	caatatatttaccatgctcccaaatcttgaattatataataatctaggtg	403	
DB	3451	ataataataataataataataataataatttataataataataataataataatg	3497	
RESULT 15				
AA208721/C				
ID	AA208721	standard; DNA; 5173 BP.		
XX				
AC	AA208721;			
XX				
DT	20-OCT-1999	(first entry)		
XX				
DE	Chimeric gene construct gz::BHL::gz designated PHP11427.			
XX				
KW	Hordeum vulgare; alpha hordothionin; HT12; modification; plant seed;			
KM	alteration; endosperm; nutrition; cereal; barley; chimeric gene; ss.			
XX				
OS	Synthetic.			
XX	Hordeum vulgare.			
XX				
PN	W09940209-A1.			
XX				
PD	12-AUG-1999.			
XX				
PF	27-JAN-1999; 99WO-US02061.			
XX				
PR	09-FEB-1998; 98US-0020716.			
XX				
PA	(P10N-) PIONEER HI-BRED INT. INC.			
XX				
PI	Beach LR, Dress VM, Ertl DS, Higgins RK, Jung R;			
PI	Ranch JP, Rao AG;			
XX				
DR	WPI; 1999-508509/42.			
XX				
PT	Plant seeds containing elevated preselected amino acid levels, used			
PT	to grow cereals			
XX				
PS	Example 2; Page 42-43; 49pp; English.			
XX				
CC	The present invention describes a transformed cereal plant seeds			
CC	endosperm having an elevated level of at least one preselected amino			
CC	acid (aa) compared to a seed from a corresponding untransformed plant,			
CC	where the aa is selected from lysine, cysteine, threonine, tryptophan,			
CC	arginine, valine, leucine, isoleucine, histidine or their combinations,			
CC	and optionally methionine, plants transformed to express a heterologous			
CC	protein that has a selected amino acid level.			

CC used to grow seeds, especially cereals, that have an endosperm with an
 CC increased content of the preselected amino acid, and therefore having an
 CC increased nutritional value. The transformed cereals can be used in feed
 CC formulations for animals. Transforming plants to have an elevated level
 CC of a preselected amino acid in the endosperm of its seed is advantageous
 CC in production of feed formulations. Feed formulations currently require
 CC supplementation with specific amino acids to provide animals with
 CC essential nutrients, which are necessary for their growth. The methods
 CC increase the nutritional content of seeds without detrimental side
 CC effects such as allergenicity or anti-nutritional quality. The
 CC nutritional content of the seeds is increased whilst maintaining a high
 CC yield. The amount of preselected amino acid in the seed is increased at
 CC least 10-20% by weight to about 10 times greater compared to a
 CC corresponding untransformed seed. The present sequence represents a
 CC chimeric gene construct produced in the construction of the HT12 gene,
 CC which is derived from the barley (*Hordeum vulgare*) alpha hordothionin
 CC gene and introduces 12 lysine residues into the mature protein.

XX
 SQ Sequence 5173 BP; 1527 A; 1154 C; 1170 G; 1322 T; 0 other:

Query Match

5.6%; Score 54.2; DB 20; Length 5173;

Best Local Similarity 65.0%; Pred. No. 0.035;

Matches 80; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

OY 152 atatatattgaacctaaatgctatgctatatccaagaatgacataaatactagaca 211
 Db 2773 ATTGCTTTAGCTCTTAGATTCTTTTCGCTATATCTAAATGGATGATTAACAAATTAGA 2714
 OY 212 tatataaacaacatacatgaatgatgtatgaatctataaataatgtaaacgactaa 271
 Db 2713 CATATACGAAACATATATCAATTATTGTATAACCTATTAAGTTAAAGTTAAACGTTAA 2654
 OY 272 tat 274
 Db 2653 TTT 2651

Search completed: September 9, 2002, 03:23:34
 Job time: 9501 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2002, 23:09:28 ; Search time 1695.72 Seconds
(without alignments)
7736.560 Million cell updates/sec

Title: US-09-763-329-1

Perfect score: 972

Sequence: 1 tagaataatgttgtat.....gcataagctgcaagcct 972

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*
1: em_estda:*
2: em_estlhum:*
3: em_estln:*
4: em_estlm:*
5: em_estor:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	91	9.4	496	9 AM120150	AM120150 614085E09
C 2	89.8	9.2	593	9 AM146803	AM146803 614085E09
C 3	89.8	9.2	658	9 AM126456	AM126456 614072D04
4	89	9.2	592	12 AZ916522	AZ916522 PstI_7_b1
5	86	8.8	509	12 BH224464	BH224464 1006119C0
6	86	8.8	536	12 BH217817	BH217817 1006059E1
C 7	82.2	8.5	589	9 AM231854	AM231854 687060B02
8	82.2	8.5	781	10 BG320733	BG320733 Zm04.06h0
C 9	81.8	8.4	933	12 BH128804	BH128804 G-3p3 Mai
10	81.4	8.4	498	10 BF728645	BF728645 1000065C0
11	78.8	8.1	548	12 BH414177	BH414177 1007036G0
12	76.4	7.9	535	10 BM267973	BM267973 MEST175-A
13	76.4	7.9	553	10 BM332810	BM332810 MEST177-H
C 14	74	7.6	583	9 A1677352	A1677352 605053H02
15	72.2	7.4	341	12 BH230702	BH230702 1006159B0
16	72	7.4	483	12 BH126949	BH126949 G-10C18.T
C 17	72	7.4	803	10 BG320273	BG320273 Zm03_12C0

18	70.8	7.3	510	12 BH127544	BH127544 G-1h6.T M
C 19	70.6	7.3	573	10 BM379373	BM379373 MEST504-F
C 20	70.4	7.2	268	12 BH623339	BH623339 1007101E0
21	70.4	7.2	621	12 BH221445	BH221445 1006101C0
22	69.6	7.2	646	12 BH374273	BH374273 AG-ND-155
23	69.4	7.1	365	12 BH218745	BH218745 1006081H0
C 24	69.4	7.1	437	12 BH128442	BH128442 G-3e7.T M
C 25	69.4	7.1	661	12 BH254946	BH254946 LDH10BAM0
26	69.2	7.1	1101	12 CNS00EVL	AL069706 1006077E0
C 27	68.8	7.1	478	12 A0844816	A0844816 an3e03 J
28	68.4	7.0	469	12 BH623526	BH623526 1007106F0
C 29	68.4	7.0	679	10 BM340927	BM340927 MEST327-G
30	68.2	7.0	306	12 BH225597	BH225597 1006127B0
C 31	68	7.0	612	9 AM000135	AM000135 614058B05
C 32	68	7.0	818	12 BH128809	BH128809 G-3p7 Mai
C 33	67.8	7.0	312	12 BH127219	BH127219 G-10118.T
C 34	67.8	7.0	875	12 BH127873	BH127873 G-2e1 Mai
C 35	67.8	7.0	963	10 BG837788	BG837788 Zm10_0590
C 36	67.8	7.0	1101	12 CNS00EVL	AL069706 Drosoph11
37	67.4	6.9	572	12 BH411224	BH411224 1006072B0
C 38	66.2	6.8	205	12 BH218171	BH218171 1006077E0
C 39	66.2	6.8	463	12 BH127288	BH127288 G-10n21.T
40	66.2	6.8	474	12 BH127387	BH127387 G-105.T M
41	66.2	6.8	529	12 BH621078	BH621078 1007104E0
42	65.8	6.8	1101	12 CNS0039G	AL069321 Drosoph11
C 43	65	6.7	560	9 A1739978	A1739978 605075B04
44	64.6	6.6	503	12 BH227306	BH227306 1006138H0
45	64.4	6.6	585	9 AM126514	AM126514 614101P07

ALIGNMENTS

RESULT 1
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LOCUS 614085E09.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA,
DEFINITION mRNA sequence.
ACCESSION AM120150
VERSION AM120150.1 GI:6095483
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 496)

REFERENCE Walbot,V.

AUTHORS Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 614085 row: E column: 09.

Location/Qualifiers

1. 496

/organism="Zea mays"

/cultivar="W23"

/db_xref="taxon:4577"

/clone_lib="614 - root cDNA library from Walbot Lab"

/tissue_type="root"

/dev_stage="3-4 days old"

/lab_host="XLOLR"

/note="Organ: root; Vector: pBluescriptII SK⁺; Site:1: EcoRI; Site:2: XhoI; 3-4 days old root tissue from Walbot Lab (LM)"

BASE COUNT 143 a 88 c 83 g 181 t 1 others

ORIGIN

[illegible]

```

COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006119 row: 44
Class: transposon-tagged.

FEATURES
Source
Location/Qualifiers
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/organism="Zea mays"
/cultivar="mixed background W23/A18/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - Rescuemu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site.1: BamHI; Site.2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmbd.iastate.edu' and follow the links for 'Rescuemu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
172 a 70 c 102 g 165 t

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Best Local Similarity	57.1%	Pred. No. 7.2e-05		
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QY	151	aataatactttagacccttaaatgtgatgctatattcaaaagaatgacaataatctagac	210	
Db	218	CAGTCATTTAACTCCTAGATTATTTATGTATATATTCATATGATGATTTACGAAGATTAAC	277	
QY	211	atataataaaaaacacatcatatgaatgatgtgtgaactatataaattgctaaacagacta	270	
Db	278	ATATATTAAGAAACAAATATCATCATCAATTAATTAATGATTTAGTAAAAAGTAAAAATGTATT	337	
QY	271	atattaaggagcggaggagtaacttatttagagattacatgttatttctctatcca	330	
Db	338	TTAATTTTGAAGACGGAGGAGTGTATTCATGTTATVAGC--TCCAATTTAATTTTATTATA	395	
QY	331	aataaagctcgggttttccaatccaatacatatataccaatgccaaacatttgaatt	390	
Db	396	AAGATATTTTCGTATTTAATCTAATAATTAATTATTGATGATCATATGACATTGATATTGG	455	
QY	391	atatactct 398		
Db	456	ATATTTC 463		
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LOCUS	BH217817			
DEFINITION	BH217817 536 bp DNA linear GSS 08-NOV-2001			
ACCESSION	BH217817			
VERSION	BH217817.1			
KEYWORDS	GSS, 16809845			

SOURCE	Zea mays.
ORGANISM	Zea mays. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE	1 (bases 1 to 536)
AUTHORS	Walbot,V.
TITLE	Maize genomic sequences found using engineered RescuerMu transposon
JOURNAL	Unpublished (2001)
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 1006059 row: 7 Class: transposon-tagged. Location/Qualifiers
FEATURES	1..536 <code>/organism="Zea mays"</code> <code>/cultivar="mixed background W23/A18/B73"</code> <code>/db_xref="taxon:4577"</code> <code>/clone_lib="1006 - RescuerMu Grid G"</code> <code>/rissue_type="leaf"</code> <code>/dev_stage="adult"</code> <code>/lab_host="DH10B"</code> <code>/note="Organ: leaf; Vector: RescuerMu (engineered from Bluescript backbone); Site:1: BamHI; Site:2: BglII; RescuerMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuerMu, go to the web site "www.zmdb.iastate.edu and follow the links for 'RescuerMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."</code>
BASE COUNT	201 a 78 g 189 t
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OY	151 aatatatttagacctaatatgcatgcctatatctcaaaaagaatgacataaacctagac 210
DB	167 CAGTCAATTAAAGCTCTAGTTTATGTATATATTGCATATGATGATTAACAAGAATAAAC 226
OY	211 aatatataaaacacatacatlaagcatcgtatgatcatactataaaaaatgcuaaacgacta 270
DB	227 ATATATATATGAACAATATCATCATTAATATATATATATATGAAATTAAGTAAAAGTGATTT 286
OY	271 atataatggagcgagggaagtagcttatatagtagatlcacatgctatttlctctaccaca 330
DB	287 TTAATTTTGACGCGAGGAGTAGTATTCATGTTTTATGGC--TCCAATTAATTTATTTATA 344
OY	331 aataaagtcgtgctttlccaalccaalabatalatatlacacatgccccaaacatltagaat 390
DB	345 AAGATATATTTTGTATTTAACTAATAATATATTTATTTGATGATCATACACATGATATTGG 404
OY	391 ataatact 398
DB	405 ATAATTTCT 412

[illegible]

ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 781)
TITLE	Singh,J.A., Makui,K., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
JOURNAL	Expressed Sequence Tags from Cold-Stressed Maize Seedlings Unpublished (2001)
COMMENT	Contact: Singh,J.A. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-food Canada 960 Carling Avenue, Bldg. 20, Ottawa, Ontario, K1A 0C6, Canada Tel.: (613) 759-1662 Fax: (613) 759-1701 Email: singhja@em.agr.ca.
FEATURES	Location/Qualifiers
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	/db_xref="taxon:4577"
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	/russus_type="Leaf, crown"
	/note="Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco RI; Site_2: Xho I; Lower temperature 50 C / hour from 22 to 12oc; Drying to 50 in 1 hour from 12oc. Leave at 50C 2 days , photoperiod 16 hours. Light intensity was 125 uE-1. Library prepared by in vivo mass excision from amplified library."
BASE COUNT	287 a 140 c 130 g 205 t 19 others
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Query Match	8.5% Score 82.2; DB 10; Length 781;
Best Local Similarity	74.5%; Pred. No. 0.00026;
Matches 102:	Conservative 1; Mismatches 34; Indels 0; Gaps 0;
OY 157	tttagacctaaatgtatgtctatactcaaaaagacgaataaacctgacatatat 216
Db 559	TTTTAGCTGTCGTGGTTTATGCTTTATTCAAAATGATGAAGAATGACACTGACACACAT 618
OY 217	ataaaaccataccatgaatgatctatgtaacatctattaagaatgcataaaggactaatla 276
Db 619	ATAAACACATPACATCACAGTGTTCTATGACCAGTAATTAACTAAAACGAATTTTAATT 678
OY 277	tggagcagagggaggtac 293
Db 679	TAGRCACAAGGAGGTAC 695
RESULT 9	
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LOCUS	G-3p3 Maize Random Small-insert Genomic Library Zea mays genomic
DEFINITION	clone G-3p3 both, DNA sequence.
ACCESSION	BH128804
VERSION	BH128804.1 GI:14996636
KEYWORDS	GSS.
ORGANISM	Zea mays.
SOURCE	Zea mays
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE	1 (bases 1 to 933)
AUTHORS	Meyers,B.C., Tingey,S.V. and Morgante,M.
TITLE	Abundance, distribution and transcriptional activity of repetitive elements in the maize genome
JOURNAL	Genome Res. 11 (10), 1660-1676 (2001)
MEDLINE	21475670
COMMENT	Contact: Morgante M Suite 200 Dupont Genomics

```

PO Box 6104, Newark, DE 19714-6104, USA
Tel: 302 631 2638
Fax: 302 631 2607
Email: Michele.morgan@eusa.dupont.com
Sequences were trimmed to include only high quality bases; forward
and reverse reads were assembled when significant overlaps were
detected.
Seq primer: M3univ and M3reverse
Class: Shotgun.

FEATURES
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            /tissue_type="leaf"
            /cell_type="Young leaf"
            /dev_stage="seedling"
            /note="Vector: PCR-Script; Total genomic DNA was nebulized
; ends were polished with Pfu polymerase and the fragments
cloned into PCR-Script."

BASE COUNT      298 a      159 c      170 g      306 t
ORIGIN

Query Match      8.4%; Score 81.8; DB 12; Length 933;
Best Local Similarity 73.8%; Pred No. 0.00029;
Matches 104; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 152 atatatagaccttaaatgtatgtctatatacaagaatgacaataactagaca 211
    || ||||| ||| || ||||| ||||| ||||| ||||| ||||| |||||
Db 440 ATTCATTTAGCTCTTCTTCTTATGCTATATCAATGAATGATGAATAACTAGACA 499

QY 212 tatataaacaacgacttaagtatgtatgtatgaatcattataaatgctaaagactaa 271
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 500 TATATCTAAACGCTATTAACCAAAAGTTGTAGAACTCACTATACCACAAAACCAATTC 559

QY 272 tattatggagcaggagagta 292
    || ||||| ||| || |||||
Db 560 TAATATGCTACAGATGAGTA 580

RESULT 10
BF728645
LOCUS BF728645 498 bp mRNA linear EST 09-JAN-2001
DEFINITION 1000065C04.xl1000 - Unigene I from Maize Genome Project Zea mays
cDNA, mRNA sequence.
ACCESSION BF728645
VERSION BF728645.1 GI:12046506
KEYWORDS EST.
SOURCE
    Zea mays.
    ORGANISM Zea mays.
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
        clade; Panicoideae; Andropogoneae; Zea.
        1 (bases 1 to 498)
        Walbot.V.
        Maize ESTs from various cDNA libraries sequenced at Stanford
        University
        Unpublished (1999)
        Contact: Walbot V
        Department of Biological Sciences
        Stanford University
        855 California Ave, Palo Alto, CA 94304, USA
        Tel: 650 723 2227
        Fax: 650 725 8221
        Email: walbot@stanford.edu
        Plate: 1000065 row: C column: 04.
        Location/Qualifiers
            1..498
                /organism="Zea mays"

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/db_xref="dbEST:707022408.x1"
/db_xref="taxon:4577"
/clone_id="1000 - U1gene1 I from Maize Genome Project"
/note="This library represents the unique ESTs found in the first round of EST sequencing at Stanford University for the maize genome project. Sequences are present from libraries 486, 487, 496, 603, 605, 606, 614, 618, 660, 683, 687, 707, and 945. Contigs were assembled using TIGR's CAP program and a representative EST from each contig was selected for the unigene set. All singlets were also selected."

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Query Match	8.4%	Score 81.4	DB 10	Length 498
Best Local Similarity	67.2%	Pred. No. 0.00041		
Matches 131	Conservative	0	Mismatches 61	Indels 3
				Gaps 1

QY	127	attatcccttaccctccctgaagtcaccataatatttagacccttaaatctgatctctatctc	186
DB	46	AATACTCCCTCCGCTCTAAATATATATAGTCACCTTGAGCTCTGATCTTATAGCTTGTC	105
QY	187	---aaagaagatgacacataactagacatatactataaacaacacatacattagattgcat	243
DB	106	ATTAAATTGATGATCATATGATCATCTAGACACATATATAAATATATATATATTTGTA	165
QY	244	gaattctatctaaagtcataaacgactaaatattatgagacgagaggaacttattagta	303
DB	166	GAACTCACTAAATAATGTATAAATGATTTTATTGTAGACGCGAGGACTACTAAACAGAG	225
QY	304	gattcattgcttatt	318
DB	226	AAAGCTAGTATATTT	240

RESULT 11			
LOCUS	BHA14177	548 bp	DNA linear GSS 12-DEC-2001
DEFINITION	1007036G06.2EL_x1 1007 - RescueMu Grid H zea mays genomic, DNA sequence.		
ACCESSION	BHA14177		
VERSION	BHA14177.1	GI:17591734	
KEYWORDS	GSS.		
SOURCE	zea mays.		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.		
	1 (bases 1 to 548)		
REFERENCE	Walbot,V.		
AUTHORS	Maze genomic sequences found using engineered RescueMu transposon		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 1007036 column: 15 Class: transposon-tagged. Location/Qualifiers 1..548 /organism="Zea mays" /cultivar="mixed background W23/A188/B7" /db_xref="taxon:4577" /clone.lib="1007 - RescueMu Grid H" /tissue_type="leaf" /dev_stage="adult" /lab_host="DH10B"		

[illegible]

RESULT	12	535 bp	mRNA	Linear	EST 18-DEC-2001
LOCUS	BM267973				
DEFINITION	BM267973				
ACCESSION	BM267973				
VERSION	BM267973.1				
KEYWORDS	EST.				
SOURCE	zea mays.				
ORGANISM	zea mays.				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC				
AUTHORS	clade: Panicoidae; Andropogoneae; Zea.				
TITLE	1 (bases 1 to 535)				
COMMENT	Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones Unpublished (2001)				
JOURNAL	Contact: Patrick S. Schnable				
COMMENT	Schnable Laboratory Iowa State University G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA Tel: 515-294-0975 Fax: 515-294-2299 Email: schnable@iastate.edu				
FEATURES	phed software, (http://depts.washington.edu/ventures/collabtr/direct/index.htm#bbrt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (">http://www.tlgr.org/softlab/>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.				
SOURCE	PCR Primers FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG) BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG) Seq primer: primer T3 (ATT AAC CCT CAC TAA AG). Location/Qualifiers 1..535 /organism="Zea mays" /cultivar="B73" /db-xref="taxon:4577"				


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VERSION      A1677352.1  GI:4886232
KEYWORDS     EST.
SOURCE       Zea mays.
ORGANISM     Zea mays.
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
REFERENCE    1 (bases 1 to 583)
AUTHORS      Walbot, V.
TITLE        Maize ESTs from various cDNA libraries sequenced at Stanford
              University
JOURNAL      Unpublished (1999)
COMMENT      Contact: Walbot V
              Department of Biological Sciences
              Stanford University
              855 California Ave, Palo Alto, CA 94304, USA
              Tel: 650 723 2227
              Fax: 650 725 8221
              Email: walbot@stanford.edu
              Plate: 605053 row: H column: 02.

FEATURES
  source
    1..583
    /organism="Zea mays"
    /cultivar="Ohio43"
    /db_xref="taxon:4577"
    /clone_id="605 - Endosperm cDNA library from Schmidt lab"
    /tissue_type="nucellar, embryo, and endosperm"
    /dev_stage="10-14 days post-pollination"
    /lab_host="DH5(alpha)"
    /note="Organ: Kernel; Vector: PAD-GAL4-2'; Site:1: EcoRI;
    Site:2: XhoI; Kernel endosperm cDNA library from Schmidt
    lab"

BASE COUNT   148 a   130 c   156 g   149 t

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 0.0063; Length 583;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tagaatatttgatgtaacgaataatgtagacatcgctgtagctatcat 60
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DB 74 TAGAATATTGTGCTGATCGAATATGATGATGATGATGATGATGATGAT 15
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QY 61 taacaataaaca 74
    |||||||
DB 14 TAACAATAAACAA 1
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RESULT 15
BH230702      341 bp      DNA      linear      GSS 08-NOV-2001
LOCUS         1006159B04.x1 1006 - Rescuemu Grid G Zea mays genomic, DNA
DEFINITION    sequence.
ACCESSION     BH230702
VERSION       BH230702.1  GI:16834165
KEYWORDS      GSS.
SOURCE        Zea mays.
ORGANISM      Zea mays.
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
              clade; Panicoidae; Andropogoneae; Zea.
REFERENCE     1 (bases 1 to 341)
AUTHORS       Walbot, V.
TITLE         Maize genomic sequences found using engineered Rescuemu transposon
              Unpublished (2001)
JOURNAL       Contact: Walbot V
              Department of Biological Sciences
              Stanford University
              855 California Ave, Palo Alto, CA 94304, USA
              Tel: 650 723 2227
              Fax: 650 725 8221
              Email: walbot@stanford.edu

```

Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.

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Plate: 1006159 row: 18
Class: transposon tagged.
Location/Qualifiers
  1..341
  /organism="Zea mays"
  /cultivar="mixed background W23/A188/B73"
  /db_xref="taxon:4577"
  /clone_id="1006 - Rescuemu Grid G"
  /tissue_type="leaf"
  /dev_stage="adult"
  /lab_host="DH10B"
  /note="Organ: leaf; Vector: Rescuemu (engineered from
  pBluescript backbone); Site:1: BamHI; Site:2: BglII;
  Rescuemu is a 4.9 Kb, modified maize Mu transposon
  designed to allow plasmid rescue from total genomic DNA.
  Mu elements insert preferentially into transcription
  units. For more information on Rescuemu, go to the web
  site 'www.zmdb.iastate.edu' and follow the links for
  'Rescuemu'. Grid G was grown at Stanford in 2000. DNA was
  extracted from leaf punches, double digested using BamHI
  and BglII, and ligated to form circular plasmids. DH10B
  cells were transformed and then screened on LB plates with
  ampicillin."

BASE COUNT   97 a   79 c   80 g   85 t

ORIGIN
Query Match
Best Local Similarity 78.7%; Pred. No. 0.015; Length 341;
Matches 111; Conservative 0; Mismatches 28; Indels 2; Gaps 2;

QY 834 gtgcgacgtacaattgtataaattatattatcccaaacctatg 892
    |||||
DB 103 GAGCAACTTAATAGTTTATCAAAATACCTTAATCAATATTAAGTTAAACCTG 162
    |||||

QY 893 tcggggaccataataggggtacccctcaaggctcctaattctcagctgtaaa-cccatc 951
    |||||||
DB 163 TCGGGGACCATTAATTAAGGGGTACCTCAAGGCTCCTAATTCTGAGACTGTAACCCCATC 222
    |||||||

QY 952 agcataaagctgcaaaagcct 972
    |||||||
DB 223 AGCATTAAGCTGCAAAAGGCT 243
    |||||||

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Search completed: September 9, 2002, 02:45:00
Job time: 12932 sec

1. The first part of the document discusses the importance of maintaining accurate records of all communications and activities. It emphasizes that this is crucial for ensuring transparency and accountability in the process.

2. The second part of the document outlines the specific steps and procedures that must be followed to ensure that all information is properly documented and stored. This includes details on how to handle sensitive information and how to ensure that all records are up-to-date and accurate.

3. The third part of the document discusses the role of the various stakeholders involved in the process, including the government, the private sector, and the public. It highlights the importance of collaboration and communication between all parties to ensure that the process is effective and efficient.

4. The fourth part of the document discusses the challenges that may be encountered during the process and provides strategies for overcoming these challenges. It emphasizes the need for flexibility and adaptability in the face of changing circumstances.

5. The fifth part of the document discusses the importance of ongoing monitoring and evaluation of the process. It highlights the need for regular reviews and assessments to ensure that the process is meeting its goals and objectives.

6. The sixth part of the document discusses the importance of maintaining the confidentiality and security of all information. It outlines the measures that must be taken to protect sensitive information from unauthorized access and disclosure.

7. The seventh part of the document discusses the importance of ensuring that the process is fair and equitable for all parties involved. It highlights the need for transparency and accountability in the decision-making process.

8. The eighth part of the document discusses the importance of ensuring that the process is efficient and effective. It outlines the measures that must be taken to streamline the process and reduce delays and costs.

9. The ninth part of the document discusses the importance of ensuring that the process is sustainable in the long term. It highlights the need for ongoing support and resources to ensure that the process can continue to operate effectively.

10. The tenth part of the document discusses the importance of ensuring that the process is adaptable to changing circumstances. It highlights the need for flexibility and adaptability in the face of new challenges and opportunities.

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 00:31:03 : Search time 49.9 Seconds
(without alignments)
4784.685 Million cell updates/sec

Title: US-09-763-329-1
Perfect score: 972
Sequence: 1 tagaataattgtgtgtat.....gcataaagctgaagcct 972

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67.8	7.0	2661	US-08-351-413-1	Sequence 1, Appl
2	67.8	7.0	2661	US-09-025-583-1	Sequence 1, Appl
3	44.4	4.6	658	US-08-998-416-595	Sequence 595, Appl
4	42.2	4.4	4427	US-08-796-101-12	Sequence 12, Appl
5	42.2	4.3	7218	US-08-232-463-14	Sequence 14, Appl
6	41.6	4.3	19124	US-08-487-8268-13	Sequence 13, Appl
7	41.2	4.2	19124	US-08-487-8268-13	Sequence 13, Appl
8	41.2	4.2	2049	US-08-417-210A-116	Sequence 116, Appl
9	41.2	4.2	2989	US-08-566-398-9	Sequence 9, Appl
10	41.2	4.2	3208	US-08-566-398-9	Sequence 51, Appl
11	41.2	4.2	3209	US-08-105-483-220	Sequence 220, Appl
12	41.2	4.2	3209	US-08-220-151-62	Sequence 62, Appl
13	41.2	4.2	3209	US-08-413-118-62	Sequence 62, Appl
14	41.2	4.2	3209	US-08-224-391-90	Sequence 90, Appl
15	41.2	4.2	3209	US-08-484-304-90	Sequence 90, Appl
16	41.2	4.2	3209	US-08-224-657-39	Sequence 39, Appl
17	41.2	4.2	3209	US-08-709-209-220	Sequence 220, Appl
18	41.2	4.2	3209	US-08-458-101-220	Sequence 220, Appl
19	41.2	4.2	3209	US-08-184-009-68	Sequence 68, Appl
20	41.2	4.2	3209	US-08-486-969-27	Sequence 27, Appl
21	41.2	4.2	3209	US-08-417-210A-66	Sequence 66, Appl
22	41.2	4.2	3209	US-08-458-356-68	Sequence 68, Appl
23	41.2	4.2	3209	US-08-471-025-27	Sequence 27, Appl
24	41.2	4.2	3209	US-08-658-665-27	Sequence 27, Appl
25	41.2	4.2	3209	US-08-473-446-62	Sequence 62, Appl
26	41.2	4.2	3209	US-08-796-101-43	Sequence 43, Appl
27	41.2	4.2	3209	US-08-460-736-68	Sequence 68, Appl

28	41	4.2	3209	US-09-085-273-27	Sequence 27, Appl
29	41	4.2	3209	US-09-354-138-39	Sequence 39, Appl
30	41	4.2	3209	PCR-US96-00547-27	Sequence 27, Appl
31	41	4.2	3460	US-08-658-665-57	Sequence 57, Appl
32	41	4.2	3460	US-08-796-101-21	Sequence 21, Appl
33	41	4.2	3460	US-09-085-273-57	Sequence 57, Appl
34	41	4.2	3622	US-08-658-665-60	Sequence 60, Appl
35	41	4.2	3622	US-08-796-101-24	Sequence 24, Appl
36	41	4.2	3622	US-09-085-273-60	Sequence 60, Appl
37	41	4.2	3750	US-08-617-860B-19	Sequence 19, Appl
38	41	4.2	4427	US-08-658-665-48	Sequence 48, Appl
39	41	4.2	4427	US-09-085-273-48	Sequence 48, Appl
40	40.6	4.2	872	US-08-998-416-487	Sequence 487, Appl
41	40.2	4.1	2096	US-08-458-084-1	Sequence 1, Appl
42	40.2	4.1	2096	US-08-205-508-1	Sequence 1, Appl
43	40.2	4.1	2096	US-08-278-630A-10	Sequence 10, Appl
44	40.2	4.1	2096	PCR-US95-02945-1	Sequence 1, Appl
45	40.2	4.1	2116	US-07-811-048-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-08-351-413-1
; Sequence 1, Application US/08351413
; Patent No. 5750867
GENERAL INFORMATION:
APPLICANT: Williams, Mark
TITLE OF INVENTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 2046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2661 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Zea mays

STRAIN: Inbred line W-22
PUBLICATION INFORMATION:
AUTHORS: Hamilton et al.
JOURNAL: Sex Plant Reprod.
VOLUME: 2
PAGES: 208-
DATE: 1989
US-08-351-413-1

Query Match 7.0%; Score 67.8; DB 1; Length 2661;
Best Local Similarity 96.4%; Pred. No. 1.7e-07;
Matches 80; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Oy 891 tctcgaggaccataattagggtaccctcaaggctcctaattctcagctggtaacc-ca 949
Db 2325 tctcgaggaccataattagggtaccctcaaggctcctaattctcagctggtaaccctca 2384
Oy 950 tcaagataaagctgcaaggcct 972
Db 2385 tcaagataaagctgcaaggcct 2407

RESULT 2

US-09-025-583-1
Sequence 1, Application US/09025583
Patent No. 5977433
GENERAL INFORMATION:
APPLICANT: Williams, Mark
APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 2046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,583
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
FILING DATE:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2661 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Zea mays
STRAIN: Inbred line W-22
PUBLICATION INFORMATION:
AUTHORS: Hamilton et al.
JOURNAL: Sex Plant Reprod.
VOLUME: 2
PAGES: 208-
DATE: 1989
US-09-025-583-1

Query Match 7.0%; Score 67.8; DB 2; Length 2661;
Best Local Similarity 96.4%; Pred. No. 1.7e-07;
Matches 80; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Oy 891 tctcgaggaccataattagggtaccctcaaggctcctaattctcagctggtaacc-ca 949
Db 2325 tctcgaggaccataattagggtaccctcaaggctcctaattctcagctggtaaccctca 2384
Oy 950 tcaagataaagctgcaaggcct 972
Db 2385 tcaagataaagctgcaaggcct 2407

RESULT 3

US-08-998-416-595
Sequence 595, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwalis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meligs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 595:
SEQUENCE CHARACTERISTICS:
LENGTH: 658 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:
ORGANISM: PAG1408RP
US-08-998-416-595

Query Match 4.68; Score 44.4; DB 4; Length 658;
Best Local Similarity 44.68; Pred. No. 0.043;
Matches 174; Conservative 0; Mismatches 216; Indels 0; Gaps 0;

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DB 259 TATTATTTTATTATTATTATTATTATTATTATTATTATTATTATT 318
QY 67 taaaagaattccctcattatcctcccccattccatttgcgaagccc 126
DB 319 TATATTTTATTATTATTATTATTATTATTATTATTATTATTATTATT 378
QY 127 atttccttactccccaagccaataatttagacccttaattgctatacc 186
DB 379 TTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 438
QY 187 aaaaagatgacaataatctagacatatataaacaacalacattagattgta 246
DB 439 TATATTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 498
QY 247 tctatlaaagtcaaaacgactaataatlgagacggaaggagtaacttattagat 306
DB 499 TTGATTTTGTGACATTAATATATATGCTATTCTATTCTATTATTATTATTATT 558
QY 307 tactgttatttctctatccaaataaagctggttlttcaatcaatataat 366
DB 559 TATTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 618
QY 367 taccatgccaacatttgaattatat 396
DB 619 TATTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 648

RESULT 4
US-08-796-101-12/c
Sequence 12, Application US/08796101
Patent No. 6183752
GENERAL INFORMATION:
APPLICANT: EPSTEIN, STEPHEN E.
APPLICANT: PINKEL, TOREN
APPLICANT: SPEIR, EDITH
APPLICANT: ZHOU, YI FU
APPLICANT: ZHU, JIANGUI
APPLICANT: ERDLE, LORNE
TITLE OF INVENTION: RESTENOSIS/ATHEROSCLEROSIS DIAGNOSIS,
TITLE OF INVENTION: PROPHYLAXIS AND THERAPY
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P. C.
STREET: 530 FIFTH AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796, 101
FILING DATE: 05-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333
TELEFAX: (212) 764-5574
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4427 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-796-101-12

Query Match 4.4%; Score 42.6; DB 4; Length 4427;
Best Local Similarity 46.2%; Pred. No. 0.18;
Matches 141; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 85 attatctttatatactcctccatccatttggcaagccattatccttactccca 144
DB 397 AATAGCATTTTATCAGATATGCTGACCCAAATTATCATGAGAGATTTCTTAAATACGTAA 338
QY 145 agtcccaatatatttagaccttaattgtagctatattcaaaagaatgacaataat 204
DB 337 TCTTATTATCTCTTGATATTCTGTAATAGTAATTTGTAAGAGTATACGATACAGTATAG 278
QY 205 ctagacataataaacaacalacattaagtaattgtaacataataaagtctaa 264
DB 277 ATATACACGATATTAATTTTAACCCATTCCTGAGTAATAATTTAGCATTTACAT 218
QY 265 cgaactaatataggaaggaagtaacttatttagtgatgaattgatttctc 324
DB 217 TTCCCTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 158
QY 325 attccaataatagctggttlttcaatcaatcaatataatataatgccaacatt 384
DB 157 TGTGTATTATTAAGCGCTGTTAGAAATAGCTTAAATATATATATATATATATATATAT 98
QY 385 tgaat 389
DB 97 GTAGT 93

RESULT 5
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:

```

1 NAME: BENT, Stephen A.
2 REGISTRATION NUMBER: 29,768
3 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: (703)836-9300
6 TELEFAX: (703)683-4109
7 TELEEX: 899149
8 INFORMATION FOR SEQ ID NO: 14:
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 7218 base pairs
11 TYPE: nucleic acid
12 STRANDEDNESS: single
13 TOPOLOGY: linear
14 IMMEDIATE SOURCE:
15 CLONE: pT99pt-F15
16 OS-08-232-463-14

```

Query Match	Score	DB 1	Length	7218
Best Local Similarity	7.68	pred. No. 0.26		
Matches 23	Conservative 156	Mismatches 124	Indels 0	Gaps 0

OY	345	ttttcaatcaataaatatatattacagtcgccaacatttgaattatattatctcgtgggc	404
Db	1479	TTCACATCTCATGTCAAGACTAGTTAAAGACGTACAGACATTGCTACRRRRRRRRRRRRR	14200
OY	405	agcatcccgtagcagatcgtaaaagaagcgtagcagtgltgtgccaaaaactaalcg	464
Db	1419	RR	13600
OY	465	cgttcgcgcgcaccttaaagattctlgaaaggaaaccaataaagcgaataaataag	524
Db	1359	RR	13000
OY	525	taatatgaactcttcctlltgaattacttagaataacaataagcaaaaagaagaga	584
Db	1299	RR	12400
OY	585	gatcaaaagttaaatcaaggcattcttgtgagaaaaacatggagacataagaatgcatgaatg	644
Db	1239	RR	11800
OY	645	tga gat	
Db	1179	RRR RRR	1177

RESULT 6
US-08-487-826B-13
; Sequence 13, Application US/08487826B
; Patent No. 5993827

GENERAL INFORMATION:
 APPLICANT: Slim, Kim L.
 APPLICANT: Chitnis, Chetan
 APPLICANT: Miller, Louis H.
 APPLICANT: Peterson, David S.
 APPLICANT: Su, Xin-zhaun
 APPLICANT: Wellens, Thomas E.
 TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe Martens Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: California
 COUNTRY: US
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

```

: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,826B
: FILING DATE: 10-SEP-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Israelsen, Ned
: REGISTRATION NUMBER: 29,655
: REFERENCE/DOCKET NUMBER: NH121.001CPI
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 235-8550
: TELEFAX: (619) 235-0176
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 19124 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: US-08-487-826B-13

```

Query Match	4.38	Score	41.6	DB	2	Length	19124
Best Local Similarity	48.18	Pred.	No. 0.45				
Matches 149; Conservative	0	Mismatches	159	Indels	2	Gaps	1

[illegible]

7
 US-08-487-826B-13/C
 Sequence 13, Application US/08487826B
 Patent No. 5993827
 GENERAL INFORMATION:
 APPLICANT: Sim, Kim L.
 APPLICANT: Chlcnis, Chetan
 APPLICANT: Miller, Louis H.
 APPLICANT: Peterson, David S.
 APPLICANT: Su, Xin-zhaun
 APPLICANT: Wellens, Thomas E.
 TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe Martens Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: California
 COUNTRY: US
 ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Isrelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13

Query Match 4.2% Score 41.2; DB 2; Length 19124;
Best Local Similarity 48.6% Pred. No. 0.56;
Matches 201; Conservative 0; Mismatches 208; Indels 5; Gaps 3;
QY 26 aalgaatgacatgcacgcgctgactcatttaacaataaagaatcttcccta 85
DB 4625 AATATACTATATGATTTATATATGATTTCCATTTTAAAGTTTTTTTGG 4566
QY 86 ttactctttatctct-cctctcatttllgcaagccattatccttacccta 144
DB 4565 TCATCAATATTTATATATACCATGATTTCAATTTATTAATAAATTAAGTAAAAAT 4506
QY 145 agtcccaatattttgagccttaattgtatctatatacaaaagaatgacaataat 204
DB 4505 ATTCTTAATATCTTTTAATATATATATTAATTAATTAATTAATTAATTAATTA 4446
QY 205 ctgacacatataaacaacacatcaatgaatgatgacatctataaagaaatgcaaaa 264
DB 4445 TTACACACAATATATTCATATATATATATTTTGAACAATTAATAAATTAATTAAT 4386
QY 265 cgactaatatctggagcgaggaagacttattagtagatacattgttattctct 324
DB 4385 TAAATAAAAAAATTTTGTGACA-TTATATGCTTAATTTTATATATTAATTAATTAAT 4327
QY 325 attcaaatataagctcgcttttcaatcaatcaatataatataatgccaacattc 384
DB 4326 ATTCTTATATATATATTTTTTAAATTTACAAATTAATGCAAAAGTTGATATGTTAAGATATCT 4267
QY 385 tgaattatatactgaagtcgacatccgctgacgacatcgtaaaagaagcaatc 438
DB 4266 ---ATTATATATATCTTACAAACATTTATTAATCAATTAATTAATAAAGCCTTAAC 4216

RESULT 8
US-08-417-210A-116/C
Sequence 116, Application US/08417210A
Patent No. 5863542
GENERAL INFORMATION:
APPLICANT: PAOLETTI, ENZO
APPLICANT: TARTAGLIA, JAMES
TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXYVIRUS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.

STREET: 530 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2690
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 2049 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-417-210A-116

Query Match 4.2% Score 41; DB 2; Length 2049;
Best Local Similarity 45.9% Pred. No. 0.36;
Matches 140; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
QY 85 attactctttatatactctccatccatttggcaagccattatccttacccta 144
DB 397 AATAGCATTTATGCATATGCTGACCAATTTATCATGACAAAGTTCTTTAAATTAAGTAA 338
QY 145 agtcccaatattttgagccttaattglaigtctatatacaaaagaatgacaataat 204
DB 337 TCTTATATCTCTTGCAATATTCGTAATAGTAATTTGAAGAGATATACGATTAACGATATG 278
QY 205 ctgacacatataaacaacacatcaatgaatgtatgataatcttaaatgcaaaa 264
DB 277 ATATACAGCATATTAATTAATTTTAACCCATTCCTAGTAATAATTAATTAATTAATTAAT 218
QY 265 cgactaatatctggagcgaggaagacttattagtagatacattgttattctct 324
DB 217 TTCCTTTATATTTTATGTTTACTTATTTGTTAGTTATACAAATTAATTAATTAATTAAT 158
QY 325 attcaaatataagctcgcttttcaatcaatcaatataatataatgccaacattc 384
DB 157 TGTGTATATTTAAAGGCTGTTAAGATTAAGCTTAACATATTAATGCTTAGCTTAT 98
QY 385 tgaat 389
DB 97 GTAGT 93

RESULT 9
US-08-566-398-9/C
Sequence 9, Application US/08566398
Patent No. 5858373
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Gettly, Russell
TITLE OF INVENTION: RECOMBINANT POXYVIRUS - FELINE INFECTIOUS
PERITONITIS VIRUS, COMPOSITIONS THEREOF, AND METHODS FOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue

STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,483
FILING DATE: 12-AUG-1993
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 220:
SEQUENCE CHARACTERISTICS:
LENGTH: 3209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-105-483-220

Query Match 4.2% Score 41; DB 1; Length 3209;

Best local Similarity 45.9% Pred. No. 0.4; Mismatches 165; Indels 0; Gaps 0;

Matches 140; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 85 atatacttttataatcctccatccatcttggcaagccatccttactcccta,144
DB 384 AATAGCATTTATCACTATGCTGATACCCATTTATCATGACAAGATTCCTTAATACGTAA 325
QY 145 agtcccaataatatttagaccttaaatgtatgtctatattcaagaagaagacaataat 204
DB 324 TCTTATTAATCTCTGCAATATTCGTAAATAGTAAAGATTAACGATTAACGATTAAG 265
QY 205 cttagacataataaacaacacacatlaagatgtatgtaatcattaaatgcttaaa 264
DB 264 ATATACACGATGATTAATTAATTAACCCATTCCTGAGTAAATAATTAACGATTAACAT 205
QY 265 cgactaataatlaaggagcgaggaagtaacttattagtaagatlaacatttacttctc 324
DB 204 TTCCCTTTATTTATTTTATTTAGTTTATTTAGTTTATTTAGTTTATTTAGTTTATTT 145
QY 325 attccaataaagcttggttttcaatcaatcaatataatataatcattgccaacaatt 384
DB 144 TGTGTATATTAAAGCGCTTAAGAAATTAAGCTTATTAACATATTTATTCCTTAGTTT 85
QY 385 tgaat 389
DB 84 GTAGT 80

RESULT 12

US-08-220-151-62/c
Sequence 62, Application US/08220151

Patent No. 5529780
GENERAL INFORMATION:
APPLICANT: Paolelli, Enzo
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD
STREET: 530 FIFTH AVENUE

CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,151
FILING DATE: 30-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 3209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-220-151-62

Query Match 4.2% Score 41; DB 1; Length 3209;

Best local Similarity 45.9% Pred. No. 0.4; Mismatches 165; Indels 0; Gaps 0;

Matches 140; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 85 atatacttttataatcctccatccatcttggcaagccatccttactcccta 144
DB 384 AATAGCATTTATCACTATGCTGATACCCATTTATCATGACAAGATTCCTTAATACGTAA 325
QY 145 agtcccaataatatttagaccttaaatgtatgtctatattcaagaagaagacaataat 204
DB 324 TCTTATTAATCTCTGCAATATTCGTAAATAGTAAAGATTAACGATTAACGATTAAG 265
QY 205 cttagacataataaacaacacacatlaagatgtatgtaatcattaaatgcttaaa 264
DB 264 ATATACACGATGATTAATTAATTAACCCATTCCTGAGTAAATAATTAACGATTAACAT 205
QY 265 cgactaataatlaaggagcgaggaagtaacttattagtaagatlaacatttacttctc 324
DB 204 TTCCCTTTATTTATTTTATTTAGTTTATTTAGTTTATTTAGTTTATTTAGTTTATTT 145
QY 325 attccaataaagcttggttttcaatcaatcaatataatataatcattgccaacaatt 384
DB 144 TGTGTATATTAAAGCGCTTAAGAAATTAAGCTTATTAACATATTTATTCCTTAGTTT 85
QY 385 tgaat 389
DB 84 GTAGT 80

RESULT 13

US-08-413-118-62/c
Sequence 62, Application US/08413118

Patent No. 5688920
GENERAL INFORMATION:
APPLICANT: PAOLETTI, ENZO
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR

CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,118
FILING DATE: 29-MAR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,151
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 3209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-413-118-62

Query Match 4.2% Score 41; DB 1; Length 3209;
Best Local Similarity 45.9% Pred. No. 0.4;
Matches 140; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 85 attatcttttataatctccctatccatcttttgcagaagccatatactcttaccctta 144
DB 384 AATAGCATTTATCATCTATGTCGTACCCATTTATCATGACAGATTCCTTTAAATACGTAA 325
QY 145 agtcccaataatatttagaagccttaaatgtaagctatataatcaaaagaatgaataa 204
DB 324 TCTTATTAATCTTTCATATTCGTATATAGTAATGTAAAGATATACGTAACATATAG 265
QY 205 ctgacatatataataaacacataatgaatgtaagctatataatcaaaagaatgaataa 264
DB 264 ATATACAGTATATTAATATTAACCCATTCGTAGTAATAATAATTACGATATTACAT 205
QY 265 cgaactaatatataaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaagga 324
DB 204 TTGCTTTATTAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 145
QY 325 attccaataataagctggtgttttcaatcaatcaatcaatcaatcaatcaatcaatcaat 384
DB 144 TGTGTATATTTAAAGCGTCTTAAGATAAGCTTACTTAACATATTATTCGTTAGCTTT 85
QY 385 tgaat 389
DB 84 GTAGT 80

RESULT 14
US-08-224-391-90/c
Sequence 90, Application US/08224391
Patent No. 5744140
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Pincus, Steven E.
TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXYVIRUS VACCINE
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford

ADDRESSEE: C/O William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,391
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/729,800
FILING DATE: 17-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2340
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 3209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-224-391-90

Query Match 4.2% Score 41; DB 1; Length 3209;
Best Local Similarity 45.9% Pred. No. 0.4;
Matches 140; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 85 attatcttttataatctccctatccatcttttgcagaagccatatactcttaccctta 144
DB 384 AATAGCATTTATCATCTATGTCGTACCCATTTATCATGACAGATTCCTTTAAATACGTAA 325
QY 145 agtcccaataatatttagaagccttaaatgtaagctatataatcaaaagaatgaataa 204
DB 324 TCTTATTAATCTTTCATATTCGTATATAGTAATGTAAAGATATACGTAACATATAG 265
QY 205 ctgacatatataataaacacataatgaatgtaagctatataatcaaaagaatgaataa 264
DB 264 ATATACAGTATATTAATATTAACCCATTCGTAGTAATAATAATTACGATATTACAT 205
QY 265 cgaactaatatataaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaagga 324
DB 204 TTGCTTTATTAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 145
QY 325 attccaataataagctggtgttttcaatcaatcaatcaatcaatcaatcaatcaatcaat 384
DB 144 TGTGTATATTTAAAGCGTCTTAAGATAAGCTTACTTAACATATTATTCGTTAGCTTT 85
QY 385 tgaat 389
DB 84 GTAGT 80

RESULT 15
US-08-484-304-90/c
Sequence 90, Application US/08484304
Patent No. 5744141
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Pincus, Steven E.
TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXYVIRUS VACCINE
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford
ADDRESS: C/O William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,304
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/224,391
FILING DATE:
APPLICATION NUMBER: US 07/729,800
FILING DATE: 17-JUL-1991
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2340
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INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 3209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-484-304-90

Query Match 4.2%; Score 41; DB 1; Length 3209;
Best Local Similarity 45.9%; Pred. No. 0.4;
Matches 140; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
OY 85 attatcttttataatcttcccatcattttgcaagccattatccttactcccta 144
DB 384 AATGACATTATCTGCTATGTCGACCAATATATCATGACAGATTCTTAAATACGTAA 325
OY 145 agtcccaatatttagaccttaattgtatgctatataatcacaagaatgacataaat 204
DB 324 TCTTATTATCTCTTGCATATTCCTATATGTAATGTAAAGAGTATACATATACGTATAG 265
OY 205 cttagacatatataaaccacacatacattagatglatgtaattcattataaagtctaaa 264
DB 264 AATATACGATGATTAATATTTTAACCCATTCCTGAGTAAATATATACATATTAAT 205
OY 265 cgactaatatagagcaggaagctacttattatagtaagattacattgttatttctct 324
DB 204 TTCCTTTTATATTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTT 145
OY 325 attccaatataagctcggttttcaatcaatcaatataatataatgctcaaacattc 384
DB 144 TGTGTATATTTAAAGCGTCGTAAAGATTAAGCTTATACATATATATGCTTAAAGCTTT 85
OY 385 tgaat 389
DB 84 GTAGT 80

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